

SEQUENCE LISTING

ACACCAATCCAAAAGCGTGGAACCTATGTTAAAAAGCTACAACATAATATT
 AATGCTATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGA
 AGGAAAAATGATTGTGGGGTTGACTTACGAAGACCCTAGTGTCAATTGTC
 AAAAAAGTGGTGCCAAATGTTTCTATTGTATATCCGACAGAAGGGACAGTT
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 AGCAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCT
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 AATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCG
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 GTAGAAATGCTGAT

SEQ ID NO. 6004

STRAIN H36B

TAAACTACTTCCACCAAAGAATTAGTTATTCTAAGTCCAAATAGTCAAG
 CCATTTTAAACAGGAACGATTCCAGCTTTTGAGGAAAAATACGGTATAAAA
 GTTAAGCTTATTCAAGGTGGGACAGGTCAACTAATAGATAGATTAAAGTAA
 GGAGGGTAAGCAGTTGAAGGCGGATATTTTCTTTGGAGGAAATTATACGC
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 CATACTGTTATTCCAGATTATATCCATCCGAGTGATACGGCGACACCTTA
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 TTACCATCAAGAGTTATGAAGATTATTACAGCCTTCCTTAAAGGTAAA
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SEQ ID NO. 6005

STRAIN 18RS21

CAGCCTTCTAACTACTTCCACCAAAGAATTAGTTATTCTAAGTCCAAA
 TAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGAGGAAAAATACG
 GTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAGA
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 TAAGGGACTTACCATCAAGAGTTATGAAGATTATTACAGCCTTCCTTAA
 AAGGTAAAATTGCCTTTGCAGATCCGAATACTTCCTCTAGTGTCTTCTCA
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 TAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCACTAAGCAT
 AAGGGCCAAATCCTTAAACCTATAATCGTATTTCGTAGAAATGCTGAT

SEQ ID NO. 6006

STRAIN M732

CAGCCTTCTAACTACTTCCACCAAAGAATTAGT
 TATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTT
 TTGAGGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGG
 CAACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATAT
 TTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTG
 AGTCTTACGTATCAAAGAATGTTCACTAGTTATTCCAGACTATATCCAT
 CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGT

SEQUENCE LISTING

AAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTAT
TACAGCCTTCCTTAAAAGGTAATAATGCTTTGTCAGATCCGAATACTTCC
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TAGAAATGCTGAT

SEQ ID NO. 6007

STRAIN COH1

CAGCCTTCTAACTACTTCCACCAAAAGAATTAGTT
ATTCTAAGTCCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTT
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TTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGA
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CGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTA
AATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATT
ACAGCCTTCCTTAAAGGTAAAATTGCCTTTGTCAGATCCGAATACCTCCT
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TGCTATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAA
GAAAAATGATTGTGGGGTTGACTTACGAAGACCCTAGTGTCAATTTGCAA
AAAAGTGGTGCCAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTT
TGTCCCCTCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAG
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GGGCAGTCAACGAGTAACCGACCTATTCGTAAAGATGCCCAAACAAGTAA
TGGCATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCT
ATGTCACCTAAGCATAAGAGCCAAATCCTTAAAACCTATAATCGCATTCGT
AGAAATGCTGAT

SEQ ID NO. 6008

STRAIN M781

CAGCCTTCTAACTACTTCCACCAAAAGAATTAGTTATT
CTAAGTCCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTTTGA
GGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAAC
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TTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTC
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GTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAAT
AACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACA
GCCTTCCTTAAAGGTAAAATTGCCTTTGTCAGATCCGAATACTTCCTCTA
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CAGTCAACGAGTAACCGACCTATTCGTAAAGATGCCCAAACAAGTAATGG
CATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCTATG
TCACTAAGCATAAGAGCCAAATCCTTAAAACCTATAATCGCATTCGTAGA
AATGCTGAT

SEQ ID NO. 6009

STRAIN CJB110

CAGCCTTTTAACTACTTCCACCAAAAGAATTAGTTATTCT
AAGTCCAAATAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTTTGAGG

SEQUENCE LISTING

AAAAATACGGTATAAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTA
ATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTTCTT
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GATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAATAA
CGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGC
CTTCCTTAAAAGGTAAAATTCCTTTGCAGATCCGAATACTTCTCTAGT
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TGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTC
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TGCTGAT

SEQ ID NO. 6010

STRAIN 1169NT

ATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGAGGAAAAATAC
GGTATAAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAG
ATTAAGTAAGGAGGGTAAGCATTGGAAGGCGGATATTTCTTGGAGGAA
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AAGAATGTTCACTACTGTTATCCAGACTATATCCATCCAAGTGATACGGC
GACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAATAACGAATTAG
CTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGCCTTCCTTA
AAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCTCTAGTGCTTTCTC
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TTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCCTAAGCA
TAAGGGCCAAATCCTTAAACCTATAATCGTATTTCGTAGAAATGCTGAT

SEQ ID NO. 6011

STRAIN JM91130013

CAGCCTTCTAACTACTTCCACAAAAGAATTAGT
TATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTT
TTGAGGAAAAATACGGTATAAAAAGTTAAGCTTATTCAAGGTGGGACAGGG
CAACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATGT
TTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTG
AGTCTTACGTATCAAAGAATGTTCACTACTGTTATCCAGACTATATCCAT
CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGT
AAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTAT
TACAGCCTTCCTTAAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCC
TCTAGTGCTTTCTCACAACCTACCAATATACTCTTGGCAAAGGGTGGTTA
CACCAATCCAAAAGCGTGGAACCTATGTTAAAAGCTACAACATAATATTA
ATGCTATCAAATCTTCTAGCTCTTCAAGAGTTTATCAATCAGTTGCAGAA
GGCAAATGATTGTGGGGCTGACTTACGAAGACCTAGTGTCAATTTGCA
AAAAAGTGGTGCCAATGTTTCTATTGTGTATCCGACAGAAGGGACAGTTT
TTGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAA
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TGGGCAGTCAACGAGTAACCGACCTATTCGTAAAGATGCCCAAACGAGTA
ATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGC
TATGTCTACTAAGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTTCG
TAGAAATGCTGAT

SEQ ID NO. 6012

SEQUENCE LISTING

STRAIN 2603 frame: 1

MKEKQSKRLIYILLVVSIIFISVFTYSISQPSKLLPPKELVILSPNSQAILTGTPAFEE
 KYGIKVKLIQGGTGQLIDRLSKEGKQLKADIFFGGNYTQFESHKALFESYVSKNVHTVIP
 DYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLLQPSLKGKIAFADPNTSSSAFSQ
 LTNILLAKGGYTNPKAWNYVKKLQHNINAIKSSSSSEVYQSVAEGKMIVGLTYEDPSVNL
 QKSGANVSIVYPTEGTVFVFPSSVAIIKNAPSMKEAKLFINFMLS LDVQNAFGQSTSNRPI
 RKDAQTSNGMKALKDIATLKEDYRYVTKHKGQILKTYNRIRRNAD

SEQ ID NO. 6013

STRAIN 090 frame: 1

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 DIFFGNYTQFESHKALFESYVSKNIHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVFPSSVAIIKNA
 PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 KGQILKTYNRIRRNAD

SEQ ID NO. 6014

STRAIN A909 frame: 1

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 DIFFGNYTQFESHKALFESYVSKNIHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVFPSSVAIIKNA
 PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 KGQILKTYNRIRRNAD

SEQ ID NO. 6015

STRAIN H36B frame: 2

KLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKADIF
 FGGNYTQFESHKALFESYVSKNIHTVIPDYIHPSDTATPYTINGSVLIVNNELVKGLTIK
 SYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVFPSSVAIIKNAPSM
 KEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKHKGQ
 ILKTYNRIRRNAD

SEQ ID NO. 6016

STRAIN 18RS21 frame: 1

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 DIFFGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVFPSSVAIIKNA
 PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 KGQILKTYNRIRRNAD

SEQ ID NO. 6017

STRAIN M732 frame: 1

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 DIFFGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVFPSSVAIIKNA
 PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 KSQILKTYNRIRRNAD

SEQ ID NO. 6018

STRAIN COH1 frame: 1

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 DIFFGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEGKMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVFPSSVAIIKNA
 PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 KSQILKTYNRIRRNAD

SEQ ID NO. 6019

STRAIN M781 frame: 1

SEQUENCE LISTING

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KSQILKTYNRIRRNAD

SEQ ID NO. 6020

STRAIN CJB110 frame: 1

QPFKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KGQILKTYNRIRRNAD

SEQ ID NO. 6021

STRAIN 1169NT frame: 3

SQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKHLKADIFFGGNYTQFESHKAL
FESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLLQPSLKGKI
AFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KGQILKTYNRIRRNAD

SEQ ID NO. 6022

STRAIN JM91130013 frame: 1

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DVFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIIKNA
PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
KGQILKTYNRIRRNAD

SEQ ID NO. 6101**STRAIN 2603**

ATGGTAAAGTTAGTGTAAGTTCTGTAGGAACCTCAAGCATCAACAGTAGCTATTTCTATG
TTTAGTCGTGTATCGGCTTTAAATGATGCAATAACAAAACCTATCATCTTTTGCAGAGGCT
GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGGAACGTAACT
CCGATGCTTCAAGGAATGATTCTTTTCTCTGAAACATTGAGTGAGAAATGTACAGAATTA
CAAACCTTATATGTCTCAATTTGTGGTGATGAGGATTTAGACTCTGTCTGTTTTAGAATCA
AAATTAGCAAGTGATAGGGCATCATTAAGATTGCTGAAGCACTTTTAGAGCATCTTAAC
GATGATCCAGAACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAATAAATTA
AAAAAACGTATAAATCTAATCAAAGAAATAGACAACCTTAATGAATTTAACGCCCAT
TCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAACTGTTAACCAAGCACTAGCG
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TCCGGACAGATGGAATGGACAAAGACAGTTAAGAAGAATTGGAAGAGCGAGAAGACGCC
AAAGCTGAAGAACTGAAAAGTAAAAGGCTGAAGAAAGTAAGAAAGCTTCAAAAATTGAA
AATACTACTAAAAAAGTAATGTTTCAGTTGATAAAAAGAAATTAATAAAGCGGCTAAT
GAAGCGTATAAATAGGAGAAATTAATAAAGATACCTATGAATCAATTATCAGTGGTTTTA
AGTAATGCATCGGCTGCCTTACTTAAAGAGGTAGCTAAATCAAATTGACTGACACAGCT
CGGCTATTGATG

SEQ ID NO. 6102

STRAIN 090

TTAAATGATGCAATAACAAAACCTATCATCTTTTGCAGAGGCT
GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGG
AACGTTAACTCGATGCTTCAAGGAATGATTCTTTTCTCTGAAACATTGA
GTGAGAAATGTACAGAATTACAAACCTTATATGTCTCAATTTGTGGTGAT
GAGGATTTAGACTCTGTCTGTTTTAGAATCAAATTAGCAAGTGATAGGGC
ATCATTAAAGATTGCTGAAGCACTTTTAGAGCATCTTAACGATGATCCAG
AACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAATAAATTA
AAAAAACGTATAAATCTAATCAAAGAAATAGACAACCTTAATGAATT
TAACGCCCATTACAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAA
CTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAAT

SEQUENCE LISTING

AGTAAACCGGAGCTTTTGGAAAACCAACATCCGGACAGATGGAATGGAC
 AAAGACAGTTAAGAAGAATTGGAAGAGCGAGAAGACGCCAAAGCTGAAG
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 AATACTACTAAAAAAGTAATGTTTCAGTTGATAAAAAGAAATTAATAAA
 AGCGGCTAATGAAGCGTATAAATTAGGAGAAATTAAAAAGATACCTATG
 AATCAATTATCAGTGGTTTAAGTAATGCATCGGCTGCCTTACTTAAAGAG
 GTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

SEQ ID NO. 6103

STRAIN 18RS21

TTAAATGATGCAATAACAAAACCTATCATCTTTTGCAGAGGC
 TGCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTG
 GAACGTTAACTCCGATCGCTTCAAGGAATGATTCTTTTCTCTGAAACATTG
 AGTGAGAAATGTACAGAATTACAAACCTTATATGTCTCAATTTGTGGTGA
 TGAGGATTTAGACTCTGTCTGTTTTAGAAATCAAAATTAGCAAGTGATAGG
 CATCATTAAGATTGCTGAAGCACTTTTAGAGCATCTTAACGATGATCCA
 GAACCTTCCAAATCTGCCATAAGTTCTACAAAAGTAATATTAATAAAT
 AAAAAACGTATAAATCTAATCAAAAGAAATTAGACAACCTTAATGAAT
 TTAACGCCCATTCAAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCA
 ACTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAA
 TAGTAAACCGGAGCTTTTGGAAAACCAACATCCGGACAGATGGAATGGA
 CAAAGACAGTTAAGGAAGAATTGGAAGAGCGAGAAGACGCCAAAGCTGAA
 GAACTGAAAAGTAAAAAGGCTGAAGAAAGTAAGAAAGCTTCAAAAATTGA
 AATACTACTAAAAAAGTAATGTTTCAGTTGATAAAAAGAAATTAATAA
 AAGCGGCTAATGAAGCGTATAAATTAGGAGAAATTAAAAAAGATACCTAT
 GAAATCAATTATCAGTGGTTTAAGTAATGCATCGGCTGCCTTACTTAAAGA
 GGTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

SEQ ID NO. 6104

STRAIN 2603 frame: 1

MVKVSVSSVGTQASTVAISMFSRVSAINDAITKLSSFEEAATLQGTAYSNAKSYATGTLT
 PMLQGMILFSETLSEKCTELQTLVVSICGDEDLDSVVLESKLASDRASLKIAEALLEHLN
 DDPEPSKSAISSSTKSNIKKLKKRIKSNQKKLDNLNEFNAHSATVFADISNAQSTVNQALA
 AVSTGFSGYNSKTGAFGKPTSGQMEWTKTVKKNWKEREDAKAEELKSKKAEESKKASKIE
 NTTKSNVSVDDKKLIKAANEAYKLGEIKKDTYESIISGLSNASAALLKEVAKSKLTDTA
 RLLM

SEQ ID NO. 6105

STRAIN 090 frame: 1

LNDAITKLSSFEEAATLQGTAYSNAKSYATGTLTPMLQGMILFSETLSEKCTELQTLVVS
 ICGDEDLDSVVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSSTKSNIKKLKKRIKS
 NQKKLDNLNEFNAHSATVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW
 TKTVMKNWKEREDAKAEELKSKKAEESKKASKIENTTTKSNVSVDDKKLIKAANEAYKLG
 EIKKDTYESIISGLSNASAALLKEVAKSKLTDARLLM

SEQ ID NO. 6106

STRAIN 18RS21 frame: 1

LNDAITKLSSFEEAATLQGTAYSNAKSYATGTLTPMLQGMILFSETLSEKCTELQTLVVS
 ICGDEDLDSVVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSSTKSNIKKLKKRIKS
 NQKKLDNLNEFNAHSATVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW
 TKTVMKNWKEREDAKAEELKSKKAEESKKASKIENTTTKSNVSVDDKKLIKAANEAYKLG
 EIKKDTYESIISGLSNASAALLKEVAKSKLTDARLLM

SEQ ID NO. 6201

STRAIN 2603

ATGATTTTAAAAATTTGTCGTCAGCATATAGTTTACAATGGGGAGGTGTTTACCAATTA
 GCTTTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAGGATAGGAGCTTTCATA
 GCTTACGAGAAACAATATAAAGAAAACTGAGATACAATGTGACGATAAACATCTCCTC
 GCAAAAATTGTTCAATTTTAAAAATACAATAGTTTACTTTTCCCTATATTCCCAAATAT
 AGAGAAGCGGCAGCTACTTTTAAAGGATGGTATTAGTTTAACTTCTGATTTTAAAGC
 CATACATGTACGATTGAACTGCAAACTAATTTTAAAGAAGGTAATCTTATCAGCA
 GTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGA
 GACCTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTAT
 CGTTTAGTAATGGAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGT

SEQUENCE LISTING

TTTAAGCCAGGGGTCAGTTTTTCATTTTACTTATCAAGATATCATCAATCATCCTGATTCT
ATTTTTGATGGTTATCATCCTGCTAAAATTAAAAATCAGCTTTCTTTAGCAGAACATTTA
GTTGCATGTGTTATCCCAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGAC
TTGAAACACAGGGTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAA
AAAGTTTATGATTTTCTTTGTCAATTTGGAAAATAAA

SEQ ID NO. 6202

STRAIN 090

TGGATTATCCTCTAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTC
ATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGATACAATGTGACGA
TAAACATCTCCTCACAAAAATTGTTCAATTTTTTAAATACAAATAGTTTTA
CTTTTCCCTATATTTCCCAAATATAGAGAAGCGGCAGCTACTTTTAAATGAG
GATGGTATTAGTTTAACTTCTGATTTTTTAAGCCATACATGTACGATTGA
AACTGCAAACTAATTTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAG
CCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCT
GGAGACCCTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATAC
CAATTCTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCAT
CTGAACAGGAGTTAACAGTAGCTTTTAAGCCAGGGGTCAGCTTTCATTTT
AATTaTCAAGATATCATCAATCATCCTGATTCTATTTTTGATGGTTATCA
TCTGCTAAAATTAAAAATCAACTTCTTTAGCAGAACATTTAGTTGCAT
GTGTTATCCCAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCTAAT
GACTTGAAACACAGAGTTTATTATTTAGATTACTGTAACGAAACACTTTA
TGAGTGGAATCAAAAAGTTTATGATTTTCTTTGTCAATTTGGAAAATAAA

SEQ ID NO. 6203

STRAIN A909

TTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATA
GGAGCTTTCATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGATACA
ATGTGACGATAAACATCTCCTCACAAAAATTGTTCAATTTTTTAAATACA
ATAGTTTTACTTTTCCCTATATTTCCCAAATATAGAGAAGCGGCAGCTACT
TTTAATGAGGATGGTATTAGTTTAACTTCTGATTTTTTAAGCCATACATG
TACGATTGAAACTGCAAACTAATTTTTAAAGAAGGTAAAATCTTATCAG
CAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGG
AATGCTGCTGGAGACCCTAAAGATTACTTTGACTATGTGATGTTGAACTG
GTCAAATACCAATTCTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCA
AAGCACCATCTGAACAGGAGTTAACAGTAGCTTTTAAGCCAGGGGTCAGC
TTTCATTTTAATTATCAAGATATCATCAATCATCCTGATTCTATTTTTGA
TGGTTATCATCCTGCTAAAATTAAAAATCAACTTCTTTAGCAGAACATT
TAGTTGCATGTGTTATCCCAAACATTATCAAGAAGATTATCAAAGCCTT
GTGCCTAATGACTTGAAACACAGAGTTTATTATTTAGATTACTGTAACGA
AACACTTTATGAGTGGAATCAAAAAGTTTATGATTTTCTTTGTCAATTTGG
AAAATAAA

SEQ ID NO. 6204

STRAIN H36B

TTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAA
CAATATAAAAGAAAAATTGAGATACAATGTGACGATAAACATCTCCTCAC
AAAAATTGTTCAATTTTTTAAATACAAATAGTTTTACTTTTCCCTATATTC
CCAAATATAGAGAAGCGGCAGCTACTTTTAAATGAGGATGGTATTAGTTTA
ACTTCTGATTTTTTAAAGCCATACATGTACGATTGAAACTGCAAACTAAT
TTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTG
CTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCTAAAGAT
TACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCG
TTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAA
CAGTAGCTTTTAAAGCCAGGGGTCAGCTTTCATTTTAATTATCAAGATATC
ATCAATCATCCTGATTCTATTTTTGATGGTTATCATCCTGCTAAAATTAA
AAATCAACTTCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAAC
ATTATCAAGAAGATTATCAAAGCCTTGTGCCTAATGACTTGAAACACAGA
GTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAA
AGTTTATGATTTTCTTTGTCAATTTGGAAAATAAA

SEQ ID NO. 6205

STRAIN 18RS21

TTGCTGGATTATCCTCGAATTAAGGCGTT

SEQUENCE LISTING

TGAATTGGAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAA
 GAAAAACTGAGATACAATGTGACGATAAACATCTCCTCGCAAAAATTGTT
 CATTTTTTAAAAATACAATAGTTTACTTTTCCCTATATTCCCAAATATAG
 AGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATT
 TTTTAAGCCATACATGTACGATTGAAACTGCAAACTAATTTTTAAAGAA
 GGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACT
 GGTAAAAGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTGACT
 ATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCGTTTAGTAATG
 GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT
 TAAGCCAGGGGTGAGTTTTTCATTTTACTTATCAAGATATCATCAATCATC
 CTGATTCTATTTTTGATGGTTATCATCCTGCTAAAATTAAAAATCAGCTT
 TCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAACATTATCAAGA
 AGATTATCAAAGCCTTGTGCCCAATGACTTGAAACACAGGGTTTATTATT
 TAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAAAGTTTATGAT
 TTTCTTTGTCTATTGGAAAATAAA

SEQ ID NO. 6206

STRAIN M732

TTGCTGGATTATCCTCGAATTAAGGCGTT
 TGAATTGGAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAA
 GAAAAACTGAGATACAATGTGACGATAAACATCTCCTCGCAAAAATTGTT
 CATTTTTTAAAAATACAATAGTTTACTTTTCCCTATATTCCCAAATATAG
 AGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATT
 TTTTAAGCCATACATGTACGATTGAAACTGCAAACTAATTTTTAAAGAA
 GGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACT
 GGTAAAAGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTGACT
 ATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCGTTTAGTAATG
 GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT
 TAAGCCAGGGGTGAGTTTTTCATTTTACTTATCAAGATATCATCAATCATC
 CTGATTCTATTTTTGATGGTTATCATCCTGCTAAAATTAAAAATCAGCTT
 TCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAACATTATCAAGA
 AGATTATCAAAGCCTTGTGCCCAATGACTTGAAACACAGGGTTTATTATT
 TAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAAAGTTTATGAT
 TTTCTTTGnCATTTGGAAAATAAA

SEQ ID NO. 6207

STRAIN COH1

TTGCTGGAT
 TATCCTCGAATTAAGGCGTTTGAATTGGAAGGATAGGAGCTTTCATAGC
 TTACGAGAAACAATATAAAAGAAAACTGAGATACAATGTGACGATAAAC
 ATCTCCTCGCAAAAATTGTTTCATTTTTTAAAAATACAATAGTTTACTTTT
 CCCTATATTCCCAAATATAGAGAAGCGGCAGCTACTTTTAATGAGGATGG
 TATTAGTTTAACTTCTGATTTTTTAAGCCATACATGTACGATTGAAACTG
 CAAAATAATTTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTTT
 AATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAGA
 CCCTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATT
 CTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCAAAGCACCATCTGAA
 CAGGAGTTAACAGTAGGTTTTAAGCCAGGGGTGAGTTTTTCATTTTACTTA
 TCAAGATATCATCAATCATCTGATTCTATTTTTGATGGTTATCATCCTG
 CTAATAATTAATAATCAGCTTTCTTTAGCAGAACATTTAGTTGCATGTGTT
 ATCCCAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGACTT
 GAAACACAGGGTTTATTATTTAGATTACTGTAAACGAAACACTTTATGAGT
 GGAATCAAAAAGTTTATGATTTTCTTTGGCATTTGGAAAATAAA

SEQ ID NO. 6208

STRAIN M781

TTGCTGGA
 TTATCCTCGAATTAAGGCGTTTGAATTGGAAGGATAGGAGCTTTCATAG
 CTTACGAGAAACAATATAAAAGAAAACTGAGATACAATGTGACGATAAA
 CATCTCCTCGCAAAAATTGTTTCATTTTTTAAAAATACAATAGTTTACTTT
 TCCCTATATTCCCAAATATAGAGAAGCGGCAGCTACTTTTAATGAGGATG
 GTATTAGTTTAACTTCTGATTTTTTAAGCCATACATGTACGATTGAAACT
 GCAAACTAATTTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTT
 TAATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAG

SEQUENCE LISTING

ACCCTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAAT
TCTGGTTATCGTTTAGTAATGGAAGATTGTTAGGCAAAGCACCATCTGA
ACAGGAGTTAACAGTAGGTTTAAAGCCAGGGGTGAGTTTTCATTTTACTT
ATCAAGATATCATCAATCATCCTGATTCTATTTTGGATGGTTATCATCCT
GCTAAAAATAAAAATCAGCTTTCTTTAGCAGAACATTTAGTTGCATGTGT
TATCCCCAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGACT
TGAAACACAGGGTTTATTATTAGATTACTGTAACGAAACACTTTATGAG
TGGAATCAAAAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6209

STRAIN CJB110

TTGCTGGATTATCCTCGAATTAAGGC
GTTTGAATTGGAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATA
AAAGAAAAATTGAGATACAATGTGACGATAAACATCTCCTCACAAAAATT
GTTTCATTTTAAAAATACAATAGTTTACTTTTCCCTATATTCCCAAATA
TAGAGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTAACTTCTG
ATTTTAAAGCCATACATGTACGATTGAAACTGCAAACTAATTTTAA
GAAGTAAAATCTTATCAGCAGTTAAAGCCTTAAATAAGCCTGCTGAAGT
ACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTG
ACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCGTTTAGTA
ATGGAAGATTGTTAGGCAAAGCACCCTGTAACAGGAGTTAACAGTAGC
TTTTAAGCCAGGGGTGAGCTTTCATTTTAATTATCAAGATATCATCAATC
ATCCTGATTCTATTTTGGATGGTTATCATCCTGCTAAAATTAAAAATCAA
CTTCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAAACATTATCA
AGAAGATTATCAAAGCCTTGTGCCTAATGACTTGAAACACAGAGTTTATT
ATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAAAGTTTAT
GATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6210

STRAIN 1169NT

AATTAAGGCGTTTGAATTGGAAGGATAGGAGCTTTCATAGCTTACGAGA
AACAATATAAAAGAAAACTGAGATACAATGTGACGATAAACATCTCCTC
GCAAAATTTGTTTCATTTTAAATACAATAGTTTACTTTTCCCTATAT
TCCCAATATAGAGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTT
TAACCTCTGATTTTAAAGCCATACATGTACGATTGAAACTGCAAACTA
ATTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTTAAATAAGCC
TGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCTAAAG
ATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTAT
CGTTTAGTAATGGAAGATTGTTAGGCAAAGCACCCTGTAACAGGAGTT
AACAGTAGGTTTAAAGCCAGGGGTGAGCTTTCATTTTACTTATCAAGATA
TCATCAATCATCCTGATTCTATTTTGGATGGTTATCATCCTGCTAAAATT
AAAAATCAGCTTTCTTTAGCAGAACATTTAGTTGCGTGTGTTATCCCAA
ACATTATCAAGAAGATTATCAAAATCTTGTGCCCAATGACTTGAAACACA
GAGTTTATTATTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAA
AAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6211

STRAIN JM9130013

ATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGAT
ACAATGTGACGATAAACATCTCCTCACAAAAATTGTTTCATTTTAAAT
ACAATAGTTTACTTTTCCCTATATTCCCAAATATAGAGAAGCGGCAGCT
ACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATTTTAAAGCCATAC
ATGTACGATTGAAACTGCAAACTAATTTTAAAGAAGGTAAAATCTTAT
CAGCAGTTAAAGCCTTAAATAAGCCTGCTGAAGTACTGGTAAATGATAAG
AGGAATGCTGCTGGAGACCCTAAAGATTACTTTGACTATGTGATGTTGAA
CTGGTCAAATACCAATTCTGGTTATCGTTTAGTAATGGAAAGATTGTTAG
GCAAAGCACCCTGTAACAGGAGTTAACAGTAGCTTTTAAAGCCAGGGGTC
AGCTTTCATTTTAAATTATCAAGATATCATCAATCATCCTGATTCTATTTT
TGATGGTTATCATCCTGCTAAAATTAAAAATCAACTTTCTTTAGCAGAAC
ATTTAGTTGCATGTGTTATCCCAAACATTATCAAGAAGATTATCAAAGC
CTTGTGCCTAATGACTTGAAACACAGAGTTTATTATTTAGATTACTGTA
CGAAACACTTTATGAGTGGAATCAAAAAGTTTATGATTTTCTTTGTCATT
TGAAAATAAA

SEQUENCE LISTING

SEQ ID NO. 6212

STRAIN 2603 frame: 1

MILKICRAAYSLQWGGVYQLALLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLL
 AKIVHFLKYNSTFPYIPKYREAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSA
 VKAFNKPAEVLVKDKRNAAGDPKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVG
 FKPGVSFHFTYQDIINHPDSIFDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPND
 LKHRVYYLDYCNETLYEWNQKVYDFLCHLENK

SEQ ID NO. 6213

STRAIN A909 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSTFPYIPKYR
 EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSI
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
 VYDFLCHLENK

SEQ ID NO. 6214

STRAIN H36B frame: 3

KAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSTFPYIPKYREAAATFN
 EDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFDY
 VMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSIFDGYHPA
 KIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQKVYDFLCH
 LENK

SEQ ID NO. 6215

STRAIN 18RS21 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSTFPYIPKYR
 EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPDSI
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
 VYDFLCHLENK

SEQ ID NO. 6216

STRAIN M732 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSTFPYIPKYR
 EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPDSI
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
 VYDFLXHLENK

SEQ ID NO. 6217

STRAIN COH1 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSTFPYIPKYR
 EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPDSI
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
 VYDFLWHLENK

SEQ ID NO. 6218

STRAIN M781 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSTFPYIPKYR
 EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPDSI
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
 VYDFLCHLENK

SEQ ID NO. 6219

STRAIN CJB110 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSTFPYIPKYR
 EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSI
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK
 VYDFLCHLENK

SEQUENCE LISTING

SEQ ID NO. 6220

STRAIN 1169NT frame: 2

IKAFELERIGAFIAYEKQYKRKTEIQCDDKHLAKIVHFLKYNSFTFPYIPKYREAAATF
NEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFD
YVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPSIFDGYHP
AKIKNQLSLAEHLVACVIPKHYQEDYQNLVPNDLKHRVYYLDYCNETLYEWNQKVYDFLC
HLENK

SEQ ID NO. 6221

STRAIN JM9130013 frame: 1

IGAFIAYEKQYKRKIEIQCDDKHLTKIVHFLKYNSFTFPYIPKYREAAATFNEDGISLT
SDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFDYVMLNWSN
TNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFTYQDIINHPSIFDGYHPAKIKNQLS
LAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQKVYDFLCHLENK

SEQ ID NO. 6222

STRAIN 090 frame: 3

DYPLIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLTKIVHFLKYNSFTFPYIPKYREA
AATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPK
DYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFTYQDIINHPSIFD
GYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQKVY
DFLCHLENK

SEQ ID NO. 6301

STRAIN 2603

ATGAAAAGTCGAAAAAAGATAAATTGGTATTGAGGTTAAACAACAACACTATTGGTTTTT
GGTTTGGGTGGGGTTGGTTTTATATAATTATAAAAAATGATAATGTCGAACCGACAGTCACT
AGTGCATCGGATCAAACGACGACTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATT
TCTAAGACCTATGATTTGTATGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCC
AGTGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA
TATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAAGATGATGGGAAAGGCAATATGACT
CAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTCACTATATGATTATGCT
GAGTTAGTATCTAGTCAAAGTATGCATCTGTTTGGAATCAAATACCTCTTCTTATAAG
GATGCTACTGCAGTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTA
AACCAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6302

STRAIN 090

GGGGTTTGGTTTTATAATTATAA
AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
ATGCATCTGTTTGGAATCAAATACCTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6303

STRAIN A909

GGGGTTTGGTTTTATAATTATAA
AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAGCTATTTTGGAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
ATGCATCTGCTTGGAATCAAATACCTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQUENCE LISTING

SEQ ID NO. 6304

STRAIN H36B

GGGGTTTGGTTTTTATAATTATAAAAAATGATA
 ATGTGGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATT
 CAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTA
 TGCGTCAGTCTTATTAGCACAAAGCTATTTTGGGAATCATCCAGTGGACAAT
 CAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA
 TATAAAGGTAAATCTGTCCAAATGCCCTACTTTAGAAGATGATGGGAAAGG
 CAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTG
 CTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGTCATCT
 GCTTGGAATCAAATACTTCTTCTTATAAGGATGCTACTGCAGCTCTAAC
 AGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTA
 TTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6305

STRAIN 18RS21

GGGGTTTGGTTTTTATAATTATAAAAAATGATAATG
 TCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA
 ACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTATGC
 GTCAGTCTTATTAGCACAAAGCTATTTTGGGAATCATCCAGTGGACAATCAG
 ATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAAATAT
 AAAGGTAAATCTGTCCAAATGCCCTACTTTAGAAGATGATGGGAAAGGCAA
 TATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTT
 CACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGTCATCTGTT
 TGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGG
 TCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTTATG
 AAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6306

STRAIN M732

GGGGTTTGGTTTTTATAATTATAA
 AAATGATAATGTGGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
 CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
 GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGGAATCATCCAG
 TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
 AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCCTACTTTAGAAGATGAT
 GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
 TTATCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
 ATGCATCTGTTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCA
 GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAA
 CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6307

STRAIN COH1

GGGGTTTGGTTTTTATAATTATAA
 AAATGATAATGTGGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
 CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
 GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGGAATCATCCAG
 TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
 AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCCTACTTTAGAAGATGAT
 GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
 TTATCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
 ATGCATCTGTTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCA
 GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAA
 CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6308

STRAIN M781

GGGGTTTGGTTTTTATAATTATAAAAAATGA
 TAATGTGGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTA
 TTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTG
 TATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGGAATCATCCAGTGGACA
 ATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAG
 AATATAAAGGTAAATCTGTCCAAATGCCCTACTTTAGAAGATGATGGGAAA

SEQUENCE LISTING

GGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTC
TGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCAT
CTGTTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCAGCTCTA
ACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAAT
TATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6309

STRAIN CJB110

GGGGTTTGGTTTTATAATTATAAAAATGATAATGT
CGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA
CGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTATGCG
TCAGTCTTATTAGCACAAAGCTATTTTGAATCATCCAGTGGACAATCAGA
TTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATATA
AAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT
ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTC
ACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCATCTGTTT
GGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT
CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTATTGA
AACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6310

STRAIN 1169NT

GGGGTTTGGTTTTATAATTATAAAAATGATAATGT
CGAACAGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA
CGATTTCCCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTATGCG
TCAGTCTTATTAGCACAAAGCTATTTTGAATCATCCAGTGGACAATCAGA
TTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATATA
AAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT
ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTC
ACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCATCTGTTT
GGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT
CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTATTGA
AACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6311

STRAIN JM9130013

TTTGGTTTTATAATTATAAAAATGATAATGTGCGAACCGACAGTCACTAGT
GCATCGGATCAAACGACGACTTTTATTCAAACGATTTCCCCAACAGCTAT
TGAAATTTCTAAGACCTATGATTTGTATGCGTCAGTCTTATTAGCACAAAG
CTATTTTGGAAATCACTCCAGTGGACAATCAGATTTGTCTAAGGCTCCTAAT
TATAACCTCTTTGGCATCAAAGGAGAATATAAAGGTAAATCTGTTCAAAT
GCCTACTTTAGAAGATGATGGGAAAGGTAATATGACCCAAATCCAAGCTC
CTTTTCGCGCCTATCCAAATTATTCTGCTTCACTATATGATTATGCTGAG
TTAGTATCTAGTCAAAAGTATGCATCTGTTTGGAAATCAAATACCTCTTC
TTATAAGGATGCTACTGCAGCTCTAACAGGTCTTTATGCGACAGATACTG
CTTATGCTAGTAAATTAAACCAAATTATTGAAAACCTACAGTCTAGATGCT
TATGATAAA

SEQ ID NO. 6312

STRAIN 2603 frame: 1

MKSRKKDKLVLRLTTTLLVFLGGVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEI
SKTYDLYASVLLAQAILLESSSQSDLSKAPNYNLEFIKGEYKGSVQMPTLEDDGKGNMT
QIQAPFRAYPNYSASLYDYAELVSSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKL
NQIETYSLDAYDK

SEQ ID NO. 6313

STRAIN 090 frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSQ
SDLSKAPNYNLEFIKGEYKGSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIETYSLDAYDK

SEQ ID NO. 6314

STRAIN A909 frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSQ

SEQUENCE LISTING

SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASAWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6315

STRAIN H36B frame: 1

GVWFFNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASAWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6316

STRAIN 18RS21 frame: 1

GVWFFNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6317

STRAIN M732 frame: 1

GVWFFNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6318

STRAIN M781 frame: 1

GVWFFNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6319

STRAIN CJB110 frame: 1

GVWFFNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6320

STRAIN 1169NT frame: 1

GVWFFNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6321

STRAIN JM9130013 frame: 3

WFNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILESSSGQSD
LSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELVSS
QKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIENYSLDAYDK

SEQ ID NO. 6401

STRAIN 2603

ATGAACAAGTCTAAGAAAATCGAAAATTATCAATTATTATTACTACAAGCGCAAGCTCTA
TTCTCAGATGAAACAAATGCTCTTGCCAACTTATCAAATGCTTCAGCTATGCTAAATGCT
ATGCTTCCAAATTCTGTATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTT
GGCCCTTTCCAGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGT
GAATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATGCTAACTAT
ATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCTATGTTAAAAATGGCAA
CTTCTAGGAGTTCTAGATTTAGATTCTTCTTTAGTAGCAGATTATGATGAGATTGATCAA
GAATACTTAGAAAAATTTGTAGGTATTCTAGTAGAACATACGATTTGGAATTTGGATATG
TTTGGAGTTGAAAAG

SEQ ID NO. 6402

STRAIN 090

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTAC
AGGCTTTTATTTATTTGATGGAAAGGAGTTAATTCTTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA
TCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC

SEQUENCE LISTING

TAACATATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTA
TGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAATTTGGATA

SEQ ID NO. 6403

STRAIN A909

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAA
CTTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTAT
TTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCTTTC
CAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGG
TGAATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGC
ATGCTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTA
CCTATGTTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTTAGATTCTTC
TTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTG
TAGGTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTT
GAAAAAG

SEQ ID NO. 6404

STRAIN H36B

CTCTATTCTCAGATGAAACAAATGCTCTTGC
CAACTTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGT
TATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCT
TTCAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGT
TGGTGAATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAA
AGCATGCTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTA
GTACCTATGTTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTTAGATT
TTCCTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAAT
TTGTAGGTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGA
GTTGAAAAAG

SEQ ID NO. 6405

STRAIN 18RS21

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTA
CAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCTTTCCAG
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
ATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCT
ATGTTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTTAGATTCTTCTTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
GTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAA
AAG

SEQ ID NO. 6406

STRAIN M732

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTA
CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGGCCCTTTTCAG
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
ATCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCC
ATGTTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTTAGATTCTTCTTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
GTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAA
AAG

SEQ ID NO. 6407

STRAIN COH1

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
TTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTT
TACAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGGCCCTTTTC
AGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGT
GAATCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCA

SEQUENCE LISTING

TGCTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTAC
CCATGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTTAGATTCTTCT
TTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGT
AGGTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTG
AAAAG

SEQ ID NO. 6408

STRAIN M781

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTA
CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTTCTGGCCCTTTTCAG
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
ATCTGCACAAACTGCTAAGACGCTGATTGTTGATGATTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCC
ATGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTTAGATTCTTCTTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
GTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAA
AAG

SEQ ID NO. 6409

STRAIN CJB110

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTAC
AGGCTTTTATTTATTTGATGGAAAGGAGTTAATTTCTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA
TCTGCACAAACTGCTAAGACGCTGATTGTTGATGATTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCTA
TGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAAA
AG

SEQ ID NO. 6410

STRAIN 1169NT

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTAC
AGGCTTTTATTTATTTGATGGAGAAGAGTTAATTTCTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA
TCTGCACAAACTGCTAAGACGCTGATTGTTGATGATTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCCA
TGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAAA
AG

SEQ ID NO. 6411

STRAIN JM9130013

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCTGTATTTAC
AGGCTTTTATTTATTTGATGGAGAAGAGTTAATTTCTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA
TCTGCACAAACTGCTAAGACGCTGATCGTTGATGATTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCTA
TGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTTGGAGTTGAAA
AG

SEQ ID NO. 6412

STRAIN 2603 frame: 1

MNKSCKIENYQLLLLQAQALFSDETNALANLSNASAMLNAMLPNSVFTGFYLF DGEELIL
GPFQGGVSCVHITLGKGVCGESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGK
LLGVLDLDDSSLVADYDEIDQEYLEKFVGILVEHTIWNLD MFGVEK

SEQ ID NO. 6413

SEQUENCE LISTING

STRAIN 090 frame: 3
LFSDETNALANLSNASAMLPNSVFTGFYLFDDGKELILGPFQGGVSCVHITLGKGC
GSAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFVVGILVEHTIWNLD

SEQ ID NO. 6414

STRAIN A909 frame: 3
LFSDETNALANLSNASAMLPNSVFTGFYLFDDGKELILGPFQGGVSCVHITLGKGC
GSAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFVVGILVEHTIWNLD

SEQ ID NO. 6415

STRAIN H36B frame: 3
LFSDETNALANLSNASAMLPNSVFTGFYLFDDGKELILGPFQGGVSCVHITLGKGC
GSAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFVVGILVEHTIWNLD

SEQ ID NO. 6416

STRAIN 18RS21 frame: 3
LFSDETNALANLSNASAMLPNSVFTGFYLFDDGKELILGPFQGGVSCVHITLGKGC
GSAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFVVGILVEHTIWNLD

SEQ ID NO. 6417

STRAIN M732 frame: 3
LFSDETNALANLSNASAMLPNSVFTGFYLFDDGKELILGPFQGGVSCVHITLGKGC
GSAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFVVGILVEHTIWNLD

SEQ ID NO. 6418

STRAIN COH1 frame: 3
LFSDETNALANLSNASAMLPNSVFTGFYLFDDGKELILGPFQGGVSCVHITLGKGC
GSAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFVVGILVEHTIWNLD

SEQ ID NO. 6419

STRAIN M781 frame: 3
LFSDETNALANLSNASAMLPNSVFTGFYLFDDGKELILGPFQGGVSCVHITLGKGC
GSAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFVVGILVEHTIWNLD

SEQ ID NO. 6420

STRAIN M781 frame: 3
LFSDETNALANLSNASAMLPNSVFTGFYLFDDGKELILGPFQGGVSCVHITLGKGC
GSAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFVVGILVEHTIWNLD

SEQ ID NO. 6421

STRAIN CJB110 frame: 3
LFSDETNALANLSNASAMLPNSVFTGFYLFDDGKELILGPFQGGVSCVHITLGKGC
GSAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFVVGILVEHTIWNLD

SEQ ID NO. 6422

STRAIN 1169NT frame: 3
LFSDETNALANLSNASAMLPNSVFTGFYLFDDGKELILGPFQGGVSCVHITLGKGC
GSAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFVVGILVEHTIWNLD

SEQ ID NO. 6423

STRAIN JM9130013 frame: 3
LFSDETNALANLSNASAMLPNSVFTGFYLFDDGKELILGPFQGGVSCVHITLGKGC
GSAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFVVGILVEHTIWNLD

SEQUENCE LISTING

SEQ ID NO. 6501

STRAIN 2603

ATGAAAAAGAGTACCCAAATAATACTACTAATAGTTGCA
TTATTTCATACCTGTTTTTAGCGGAGGATTTTATATGAAAGAACAACAAAGAAAAGAAGAA
CTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATTGAAAAATTCCTATGAG
AATATAGAAGAAATAAAAAATCACACATCCTGTTTCAACTGAAATTCCTGGAGATTGGCAT
TGTAATGTAAAGATTTCAATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAAT
TTGGAATCGAAAAAAATTTATAGCGGAAAATTTAATGAAAAAAATATGAATTTTTTTGAT
TCAAGAATTGGTAAAACAAAAAAACTATAAAAAATTATTTTTTCAGATGGTCAGGAGAAG
ATACAA

SEQ ID NO. 6502

STRAIN 090

GGAGGATTTTATATGAAAGAACA
ACAAAGAAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAG
TCAAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAAATCACACATC
CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGAT
TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG
AATCGAAAAAAATTTATAGCGGAAAATTTAATGAAAAAAATATGAATTTT
TTTGATTCAAGAATTGGTAAAACAAAAAAACTATAAAAAATTATTTTTTC
AGATGGtCAGGAGAAGATaCAA

SEQ ID NO. 6503

STRAIN A909

GGAGGATTTTATATGAAAGAACAACAA
AGAAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAA
AGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAAATCACACATC
CTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCA
TTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATC
GAAAAAAATTTATAGCGGAAAATTTAATGAAAAAAATATGAATTTTTTG
ATTCAAGAATTGGTAAAACAAAAAAACTATAAAAAATTATTTTTTCAGAT
GGtCAGGAGAAGATACAA

SEQ ID NO. 6504

STRAIN H36B

GGAGGATTTTATATGAAAGAACA
ACAAAGAAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAG
TCAAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAAATCACAC
CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGAT
TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG
AATCGAAAAAAATTTATAGCGGAAAATTTAATGAAAAAAATATGAATTTT
TTTGATTCAAGAATTGGTAAAACAAAAAAACTATAAAAAATTATTTTTTC
AGATGGtCAGGAGAAGATaCAA

SEQ ID NO. 6505

STRAIN 18RS21

GGAGGATTTTATATGAAAGAACAAC
AAAGAAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTC
AAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAAATCACACA
TCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTT
CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA
TCGAAAAAAATTTATAGCGGAAAATTTAATGAAAAAAATATGAATTTTTT
TGATTCAAGAATTGGTAAAACAAAAAAACTATAAAAAATTATTTTTTCAG
ATGGtCAGGAGAAGATaCAA

SEQ ID NO. 6506

STRAIN M781

GGAGGATTTTATATGAAAGAACAACAAAGAAAA
GAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATT
GAAAAATTCCTATGAGAATATAGAAGAAATAAAAAATCACACATCCTGTTT
CAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCAATTTAAT
GATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATCGAAAAA
AAATTATAGCGGAAAATTTAATGAAAAAAATATGAATTTTTTTGATTCAA

SEQUENCE LISTING

GAATTGGTAAAAACAAAAAACTATAAAAAATTATTTTTTCAGATGGTCAG
GAGAAGATACAA

SEQ ID NO. 6507

STRAIN CJB110

GGAGGATTTTATATGAAAGAACAACAAAGAAAAGAAGAA
CTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATTGAAAAA
TTCCTATGAGAATATAGAAGAAATAAAAAATCACACATCCTGTTTCAACTG
AAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCAATTAATGATAAA
AAATCTATTGTTTATAATATTACACATAATTTGGAATCGAAAAAAATTA
TAGCGGAAATTTTAAATGAAAAAAATATGAATTTTTTTGATTCAAGAATTG
GTAAAACAAAAAACTATAAAAAATTATTTTTTCAGATGGTCAGGAGAAG
ATACAA

SEQ ID NO. 6508

STRAIN 1169NT

GGAGGATTTTATATGAAAGAACAACAAAG
AAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAG
CATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAAATCACACATCCT
GTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTTCATT
TAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATCGA
AAAAAAATTATAGTGGAAAAATTTAATGAAAAAAATATGAATTTTTTTGAT
TCAAGAATTGGTAAAACAAAAAACTATAAAAAATTATTTTTTCAGATGG
TCAGGAGAAGATACAA

SEQ ID NO. 6509

STRAIN JM9130013

GGAGGATTTTATATGAAAGAACAAC
AAAGAAAAGAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTC
AAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAAATCACACA
TCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTT
CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA
TCGAAAAAAATTTATAGCGGAAAAATTTAATGAAAAAAATATGAATTTTTT
TGATTCAAGAATTGGTAAAACAAAAAACTATAAAAAATTATTTTTTTCAG
AtGGtCAGGAGAAGATACAA

SEQ ID NO. 6510

STRAIN 2603 frame: 1

MKKSTQIILLIVALFILVFSGGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKI
THPVSTEIPGDWHCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTK
KTIKIIFSDGQEKIQ

SEQ ID NO. 6511

STRAIN 090

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD
WHCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKKTIKIIFSDGQ
EKIQ

SEQ ID NO. 6512

STRAIN A909

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWH
CTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKKTIKIIFSDGQ
IQ

SEQ ID NO. 6513

STRAIN H36B

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD
WHCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKKTIKIIFSDGQ
EKIQ

SEQ ID NO. 6514

STRAIN 18RS21

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDW
HCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKKTIKIIFSDGQ

SEQUENCE LISTING

KIQ

SEQ ID NO. 6515

STRAIN CJB110

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVK
ISFNDKKSIVYNITHNLESKKNYSGNFNEKNMNFDSRIGTKKTIKIIFSDGQEKIQ

SEQ ID NO. 6516

STRAIN JM9130013

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDW
HCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGTKKTIKIIFSDGQEKIQ

SEQ ID NO. 6517

STRAIN 1169NT frame: 1

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF
NDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGTKKTIKIIFSDGQEKIQ

SEQ ID NO. 6518

STRAIN M781 frame: 1

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF
NDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGTKKTIKIIFSDGQEKIQ

SEQ ID NO. 6601

STRAIN 2603

TTGACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAACTATG
GAAATACTGATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAAAGCAGCGCTT
ACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAG
GATCCTAGATTAACTTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAA
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATCAACTAGAT
GAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCTGTACAAAAATCAAATACCA
AAGTTAGTTTATATTTCAGCCAACAGCGGCTATTTCAGCTTACATTAAAGTAAAAGGAAG
GCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTTGTAGACCAGGTTTGATG
TATGGTGAAGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCAT
TTGCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAATAAGGTTGTGATAGTGGCA
GAAGCAATCGTTACTACGCTTAGGAAAAAACCACCCAAAAAATCCTTCTATTGAAGAA
TTAAATAATAAA

SEQ ID NO. 6602

STRAIN 090

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAAT
GAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTT
AGGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT
ACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTA
ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGA
CAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATC
AAGTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCTGT
CACAAAAATCAAATACCAAAGTTAGTTTATATTTTCAGCCAACAGCGGCTA
TTCAGCTTACATTAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAA
GCGGTCTGGATTATCTTTTGTAGACCAGGTTTGATGTATGGTGAAGAG
CGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCATTT
GCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAATAAGGTTGTGA
TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCACCCAAAAA
ATCCTTTCTATTGAAGAATTAATAATAATAAA

SEQ ID NO. 6603

STRAIN A909

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAATG
AAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTTA
GGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTA
CTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTAA
CCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGAC
AGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATCA
ACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCTGTC

SEQUENCE LISTING

ACAAAAATCAAATACCAAAGTTAGTTTATATTTTCAGCCAACAGCGGCTAT
 TCAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAAG
 CGGTCTGGATTATCTTTTGTAGACCAGGTTTGATGTATGGTGAAGAGC
 GACCTCTCTCGATTTTCCAAGCCAAGTGATAAAGTTATTTAGTCATTTG
 CCTTCTTAGGTATTGTTGTACAAAAGGTCTTCCAACCTAAGGTTGTGAT
 AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACAACCCAAAAAA
 TCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6604

STRAIN H36B

TATAAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAACATATGG
 AAATACTGATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAAAA
 GCAGCGCTTACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGG
 TAAAGGTGATATATTTAAGGATCCTAGATTAACCTACATTAGGGGAGATA
 TTACAGAAGCTGATAAGATTCAATTTAGAAGACAGAACTTTTGATATATTA
 ATTGACTGTATTGGAGCGATTAAAGCCCAATCAACTAGATGAGCTTAACGT
 TAAAGCAACCCAAAAAGCAGTAGCACTCTGTACAAAAATCAAATACCAA
 AGTTAGTTTATATTTTCAGCCAACAGCGGCTATTACGCTTACATTAAAAGT
 AAAAGGAAGGCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTT
 TGTAAAGACCAGGTTTGATGTATGGTGAAGAGCGACCTCTCTCGATTTTCC
 AAGCCAAGTGTATAAAGTTATTTAGTCATTTGCCTTTCTTAGGTATTGTT
 GTACAAAAGGTCCTTCCAACCTAAGGTTGTGATAGTGGCAGAAGCAATCGT
 TACTACGCTTAGGAAAAAACAACCCAAAAAATCCTTTCTATTGAAGAAT
 TAAATAATAAA

SEQ ID NO. 6605

STRAIN 18RS21

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAAT
 GAAGGAGAGGGAACATATGGAAATCTGATTGCAGGTGGTAGTGGTTTTTT
 AGGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT
 ACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTA
 ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGA
 CAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATC
 AACTAGATGAGCTTAAAGTAAAGCAACCCAAAAAGCAGTAGCACTCTGT
 CACAAAAATCAAATACCAAAGTTAGTTTATATTTTCAGCCAACAGCGGCTA
 TTCAGCTTACATTAAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAA
 GCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAG
 CGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCATTT
 GCCTTTCTTAGGTATTGTTGTACAAAAGGTCCTTCCAACCTAAGGTTGTGA
 TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACAACCCAAAAAA
 ATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6606

STRAIN M732

CAAAATGAAGGAGAGGGAACATATGgAAATACTGATTGCAGGTGGTAGTGG
 TTTTCTAGGGAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAGG
 TGGCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCT
 AGATTAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCAATTT
 AGaACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGC
 CCAATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCA
 CTCTGTACAAAAATCAAATACCAAAGTTAGTTTACATTTTCAGCCAATAG
 CGGCTATTTCAGCTTACATTAAAAGTAAAGGAAGGCAGAGCAGATAATCA
 AAGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGT
 GAAGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAATTTATTTAG
 TCATTTGCCTTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACCTAAGG
 TTGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAAACAACCT
 CAAAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6607

STRAIN COH1

ACAAGGCATATAAAAAATTTCTATACTAAATTTAC
 AAAATGAAGGAGAGGGAACATATGGAAATCTGATTGCAGGTGGTAGTGGT
 TTTCTAGGGAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAGGT
 GGCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCTA

SEQUENCE LISTING

GATTAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCATTTA
GAACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAGCC
CAATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCAC
TCTGTACAAAAATCAAATACCAAAGTTAGTTTACATTTAGCCAAATAGC
GGCTATTAGCTTACATTAAGTAAAGGAAGGCAGAGCAGATAATCAA
AGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTG
AAGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGATAAAATTATTTAGT
CATTTGCCTTTCTTAGGTATTGTTGTACAAAAAGTCTTTCCAACTAAGGT
TGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAAACCAACTC
AAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6608

STRAIN M781

ACAAGGCATATAAAAAATTTcTATACTAAATTTaCA
AAATGAAGGAGAGGGAAGCTATGGAATACTGATTGCAGGTGGTAGTGGTT
TTCTAGGGAAGCAGATAATAAAGCAGCGCTTACAAAGGGCATAAGGTG
GCTTACTTATCAAGGCATGAAGGTAAGGTGATATATTTAAGGATCCTAG
ATTAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCATTTAG
AACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAGCCC
AATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACT
CTGTACAAAAATCAAATACCAAAGTTAGTTTACATTTAGCCAAATAGCG
GCTATTAGCTTACATTAAGTAAAGTAAAGGAAGGCAGAGCAGATAATCAA
GCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGA
AGAGCGACCTCTCTCGATTTTCCAAGCCAAGTGATAAAATTATTTAGTC
ATTTGCCTTTCTTAGGTATTGTTGTACAAAAAGTCTTTCCAACTAAGGTT
GTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAAACCAACTCA
AAAAATCCTTTCTATGAAGAATTAAATAATAAA

SEQ ID NO. 6609

STRAIN 1169NT

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAA
ATGAAGGAGAGGGAAGCTATGGAATACTGATTGCAGGTGGTAGTGGTTTT
TTAGGAAAGCAGATAATAAAGCAGCGCTTACAAAGGGCATAAGTTGGC
TTACTTATCAAGACATGAAGGTAAGGTGATATATTTAAGGATCCTAGAT
TAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAA
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCAA
TCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCT
GTACAAAAATCAAATACCAAAGTTAGTTTACATTTAGCCAAACAGCGGC
TATTCAGCTTACATTAGAAGTAAAGGAAGGCAGAGCAGATAATCAAAGC
AAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAG
AGCGACCTCTCTCGATTTTCCAAGCCAAGTGATAAAATTATTTAGTCAT
TTGCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGT
GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACTCAA
AAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6610

STRAIN CJB110

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAA
ATGAAGGAGAGGGAAGCTATGGAATACTGATTGCAGGTGGTAGTGGTTTT
TTAGGAAAGCAGATAATAAAGCAGCGCTTACAAAGGGCATAAAGTGGC
TTACTTATCAAGACATGAAGGTAAGGTGATATATTTAAGGATCCTAGAT
TAACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAA
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCAA
TCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCT
GTACAAAAATCAAATACCAAAGTTAGTTTATATTTAGCCAAACAGCGGC
TATTCAGCTTACATTAAGTAAAGGAAGGCAGAGCAGATAATCAAAGC
AAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAG
AGCGACCTCTCTCGATTTTCCAAGCCAAGTGATAAAGTTATTTAGTCAT
TTGCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGT
GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAA
AAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6611

STRAIN JM9130013

SEQUENCE LISTING

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAAATG
 AAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTTA
 GGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTA
 CTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTAA
 CcTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGAC
 AGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAATCA
 ACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGTC
 ACAAAAATCAAATACCAAAGTTAGTTTATATTTTCAGCCAACAGCGGCTAT
 TCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAAG
 CGGTCTGGATTATCTTTTTGTAAGACCAGGTTTGATGTATGGTGAAGAGC
 GACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCATTTG
 CCTTTCTTAgtTATTGTACAAAAGGTCTTTCCAAGTAAAGTTGTGAT
 AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA
 TCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6612

STRAIN 2603 frame: 1

TRHIKISILNLQNEEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
 PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIPKNQDELNVKATQKAVALCHKNQIPK
 LVYISANSYGSAIYKSKRKAQEIICASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFPKVVIVAEAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6613

STRAIN 090 frame: 1

TRHIKISILNLQNEEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
 PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIPKNQDELNVKATQKAVALCHKNQIPK
 LVYISANSYGSAIYKSKRKAQEIICASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFPKVVIVAEAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6614

STRAIN A909 frame: 1

TRHIKISILNLQNEEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
 PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIPKNQDELNVKATQKAVALCHKNQIPK
 LVYISANSYGSAIYKSKRKAQEIICASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFPKVVIVAEAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6615

STRAIN H36B frame: 2

IKISILNLQNEEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKDPRL
 TYIRGDITEADKIHLEDRTFDILIDCIGAIPKNQDELNVKATQKAVALCHKNQIPKLVY
 ISANSYGSAIYKSKRKAQEIICASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHLPFL
 GIVVQKVFPKVVIVAEAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6616

STRAIN 18RS21 frame: 1

TRHIKISILNLQNEEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
 PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIPKNQDELNVKATQKAVALCHKNQIPK
 LVYISANSYGSAIYKSKRKAQEIICASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFPKVVIVAEAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6617

STRAIN M732 frame: 1

QNEEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKDPRLTYIKGDIT
 EADKIHLEHRNFDILIDCIGAIPKNQDELNVKATQKAVALCHKNQIPKLVYISANSYG
 SAIYKSKRKAQEIICASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHLPFLGIVVQKV
 PTKVVIVAEAIVTSRKKPTQKILSIEELNNK

SEQ ID NO. 6618

STRAIN COH1 frame: 1

TRHIKISILNLQNEEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
 PRLTYIKGDITEADKIHLEHRNFDILIDCIGAIPKNQDELNVKATQKAVALCHKNQIPK
 LVYISANSYGSAIYKSKRKAQEIICASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFPKVVIVAEAIVTSRKKPTQKILSIEELNNK

SEQUENCE LISTING

SEQ ID NO. 6619

STRAIN M781 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIKFD
 PRLTYIKGDITEADKIHLEHRNFDILIDCIGAIPKPNQLDELNVKATQKAVALCHKNQIPK
 LVYISANSYGYSAYIKSKRKAQEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFPPTKVIVIVAEIAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6620

STRAIN 1169NT frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKLAYLSRHEGKGDIKFD
 PRLTYIKGDITEADKIHLEDRFTDILIDCIGAIPKPNQLDELNVKATQKAVALCHKNQIPK
 LVYISANSYGYSAYIRSKRKAQEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFPPTKVIVIVAEIAIVTTLRKTPTQKILSIEELNNK

SEQ ID NO. 6621

STRAIN CJB110 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIKFD
 PRLTYIRGDITEADKIHLEDRFTDILIDCIGAIPKPNQLDELNVKATQKAVALCHKNQIPK
 LVYISANSYGYSAYIKSKRKAQEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFPPTKVIVIVAEIAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6622

STRAIN JM9130013 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIKFD
 PRLTYIRGDITEADKIHLEDRFTDILIDCIGAIPKPNQLDELNVKATQKAVALCHKNQIPK
 LVYISANSYGYSAYIKSKRKAQEQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFPPTKVIVIVAEIAIVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6701

STRAIN 090

CAATAACAACATTTGAAAATAAAAAAGTTTTAGTCCTTGTTTAGCACGA
 TCTGGAGAAGCCGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGAC
 AGTTAATGATGGCAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGT
 TGGAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAAATTGTTA
 GATGAGGATTTTTGTTACATGATTAAAAATCCAGGAATACCTTATAACAA
 TCCATATGGTCAAAAAAGCATTAGAAAAACAAATCCCTGTTTTGACTGAAG
 TGGAATTAGCATACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGC
 TCTAACGGGAAAACGACAACGACAACGATGATTGCAGAAGTCTTAAATGC
 TGGAGGTGAGAGAGGTTTGTAGCTGGGAATATCGGCTTTCTCTGCTAGTG
 AAGTTGTTTCAGGCTGCGGATGATAAAGATATTCTAGTTATGGAATTATCA
 AGTTTTTCAGCTAATGGGAGTTAAGGAATTTCTGCTCATATTGCAGTAAT
 TACTAATTTAATGCCAACTCATTAGATTATCATGGGTCTTTTGAAGATT
 ATGTTGCTGCAAAATGGAATATCCAAATCAAATGTCTTCATCTGATTTT
 TTGGTACTTAATTTAATCAAGGTATTTCTAAAGAGTTAGCTAAAACCTAC
 TAAAGCAACAATCGTTCCTTTCTCTACTACGGAAAAAGTTGATGGTGCTT
 ACGTACAAGACAAGCAACTTTTCTATAAAGGGGAGAAATATTATGTTAGTA
 GATGACATTGGTGTCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAAC
 TATTGCGGTTGCTAAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAA
 CTTTAAGCAATTTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAG
 GTTCATGGTATTAGTTTCTATAACGACAGCAAGTCAACTAATATATTGGC
 AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG
 CAGGAGGTCTTGATCGCGGTAATGAGTTTGATGAATTGATACCAGATATC
 ACTGGACTTAAACATATGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAA
 ACGTGCTGCACAAAAAGCAGGAGTAACCTATAGCGATGCTTTAGATGTTA
 GAGATGCGGTACATAAAGCTTATGAGGTGGCACAAACAGGGCGATGTTATC
 TTGCTAAGTCCTGCAAATGCATCATGGGACATGTATAAGAATTTGGAAGT
 CCGTGGTGATGAATTCATTGATACCTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6702

STRAIN A909

CAATAACAACATTTGAAAATAAAAAAGTTTTAGTCCTTGTTTAGCACGA
 TCTGGAGAAGCTGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGAC
 AGTTAATGATGGCAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGT
 TGGAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAAATTGTTA

SEQUENCE LISTING

GATGAGGATTTTTGTTACATGATTAAAAATCCAGGAATACCTTATAACAA
TCCTATGGTCAAAAAAGCATTAGAAAAACAAATCCCTGTTTTGACTGAAG
TGGAATTAGCATACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGC
TCTAACGGGAAAACGACAACGACAACGATGATTGCAGAAGTCTTAAATGC
TGGAGGTGAGAGAGGTTTGTAGCTGGGAATATCGGCTTTCCTGCTAGTG
AAGTTGTTTCAGGCTGCGAATGATAAAGATACCTAGTTATGGAATTATCA
AGTTTTTCAGCTAATGGGAGTTAAGGAATTCGTCCTCATATTGCAGTAAT
TACTAATTTAATGCCAACTCATTAGATTATCATGGGTCTTTTGAAGATT
ATGTTGCTGCAAAATGGAATATCCAAAATCAAATGTCTTCATCTGATTTT
TTGGTACTTAATTTAATCAAGGTATTTCTAAAGAGTTAGCTAAACTAC
TAAAGCaACAATCGTTCCTTTCTCTACTACGGAAAAAGTTGATGGTGCTT
ACGTACAAGACAAGCAACTTTTCTATAAAGGGGAGAATATTATGTCAGTA
GATGACATTGGTGTCCCAGGAAGCCATAACGTAnAGAATGCTCTAGCAAC
TATTGCGGTTGCTAAACTGGCTGGTATCAGTAATCAAGTTATTAgAGAAA
CTTTAAGCAATTTTGGAGGtGTTAAACACCGCTTGCAATCACTCGGTAAG
GTTTCATGGTATTAGTTTCTATACGACAGCAAGTCAACTAATATATTGGC
AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG
CAGGAGGTCTTGATCGCGGTAATGAGTTTGATGAATTGATACCAGATATC
ACTGGACTTAAACATATGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAA
ACGTGCTGCACAAAAAGCAGGAGTAACTTATAGCGATGCTTTAGATGTTA
GAGATGCGGTACATAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATC
TTGCTAAGTCCTGCAATGCATCATGGGACATGTATAAGAATTCGAAGT
CCGTGGTGATGAATTCATTGATACTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6703

STRAIN H36B

GGACGAGTAATGAAAACAATAACAACATTTGAAAAT
AAAAAAGTTTTAGTCCTTGGTTTAGCACGATCTGGAGAAGCTGCTGCACG
TTTGTTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACCAT
TTGATGAAAATCCAACAGCACAGTCTTTGTGGAAGAGGGTATTAAAGTG
GTTTGTGGTAGTATCTCCTTTAGAATTGTTAGATGAGGATTTTTGTTACAT
GATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAAGCAT
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TCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACGACAAC
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SEQ ID NO. 6704

STRAIN 18RS21

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SEQUENCE LISTING

AATCAAGGTATTTCTAAAGAGTTAGCTAAAAC TACTAAAGCAACAATCGT
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SEQ ID NO. 6705

STRAIN M732

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SEQ ID NO. 6706

STRAIN COH1

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SEQUENCE LISTING

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SEQ ID NO. 6707

STRAIN M781

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SEQ ID NO. 6708

STRAIN CJB110

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 CCTTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGCA
 ACTTTTCTATAAAGGGGAGAATATTATGTTAGTAGATGACATTGGTGTC
 CAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTGCTAAA

SEQUENCE LISTING

CTAGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTGG
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ATTGATACTTTTCAAGTCTTAGAGGAGAG

SEQ ID NO. 6709

STRAIN 1169NT

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SEQ ID NO. 6710

STRAIN JM9130013

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CATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTT
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SEQ ID NO. 6710

STRAIN 2603

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SEQ ID NO. 6711

STRAIN 090 frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGIKVVCGS
 HPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIGITGSNGK
 TTTTMMIAEVLNAGGQRLLAGNIGFPASEVVQAADDKDILVMELSSFQLMGVKEFRPHI
 AVITNLMPTHLDYHGSFEDYVAAKWNINQMSSSDFLVLFNFNQISKELAKTTKATIVPF
 STTEKVDGAYVQDKQLFYKGENIMLVDDIGVPGSHNVENALATIAVAKLAGISNQVIRET
 LSNFEGGVKHLRQLSGKVHGISFYNDKSTNILATQKALSGFDNTKVILIAGGLDRGNEFD
 ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGDVILLSP
 ANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6712

STRAIN A909 frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGIKVVCGS
 HPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIGITGSNGK
 TTTTMMIAEVLNAGGQRLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVKEFRPHI
 AVITNLMPTHLDYHGSFEDYVAAKWNINQMSSSDFLVLFNFNQISKELAKTTKATIVPF
 STTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVXNALATIAVAKLAGISNQVIRET
 LSNFEGGVKHLRQLSGKVHGISFYNDKSTNILATQKALSGFDNTKVILIAGGLDRGNEFD
 ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGDVILLSP
 ANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6713

STRAIN H36B frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI

SEQUENCE LISTING

KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQFIGI
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
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QVIRETLSNFGGVKHLRLQSLGKVHGHSFYNDKSTNIALATQKALSGFDNTKVILIAGGLD
RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6714

STRAIN 18RS21 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQFIGI
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVNLFNQGISKEKAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIIVAKLAGISN
QVIRETLSNFGGVKHLRLQSLGKVHGHSFYNDKSTNIALATQKALSGFDNTKVILIAGGLD
RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6715

STRAIN M732 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQFIGI
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDILVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVNLFNQGISKEKAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIIVAKLAGISN
QVIRETLSNFGGVKHLRLQSLGKVHGHSFYNDKSTNIALATQKALSGFDNTKVILIAGGLD
RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6716

STRAIN COH1 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQFIGI
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDILVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVNLFNQGISKEKAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIIVAKLAGISN
QVIRETLSNFGGVKHLRLQSLGKVHGHSFYNDKSTNIALATQKALSGFDNTKVILIAGGLD
RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFE

SEQ ID NO. 6717

STRAIN M781 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQFIGI
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDILVMELSSFQLMGVK
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QVIRETLSNFGGVKHLRLQSLGKVHGHSFYNDKSTNIALATQKALSGFDNTKVILIAGGLD
RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6718

STRAIN CJB110 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQFIGI
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDILVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDDYHGSFEYVAAKWNIONQMSSSDFLVNLFNQGISKEKAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMLVDDIGVPGSHNVENALATIIVAKLAGISN
QVIRETLSNFGGVKHLRLQSLGKVHGHSFYNDKSTNIALATQKALSGFDNTKVILIAGGLD
RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6719

STRAIN 1169NT frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEGIKVVCGS

SEQUENCE LISTING

HPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGITGSNGK
TTTTTMTIAEVLNAGGQGRGLLAGNIGFPASEVVAADDKDTLVMELSSFQLMGVKEFRPHI
AVITNLMPTHLDYHGSFEDYVAAKWNINQMSSSDFVLNFNQGISKELAKTTKATIVPF
STTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISNQVIRET
LSNFGGVKHLRLQSLGKVHGISFYNDKSTNILATQKALSGFDNTKVILIAGGLDRGNEFD
ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSNALDVRDAVHKAYEVAQQGDVILXSP
ANASWDMYKNFEVRGDEFIDTF

SEQ ID NO. 6720

STRAIN JM9130013 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGI
TGSNGKTTTTTTMTIAEVLNAGGQGRGLLAGNIGFPASEVVAANDKDTLVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNINQMSSSDFVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHLRLQSLGKVHGISFYNDKSTNILATQKALSGFDNTKVILIAGGLD
RSNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSNALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6721

STRAIN 2603 frame: 1

GRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGI
TGSNGKTTTTTTMTIAEVLNAGGQGRGLLAGNIGFPASEVVAANDKDTLVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNINQMSSSDFVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHLRLQSLGKVHGISFYNDKSTNILATQKALSGFDNTKVILIAGGLD
RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSNALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6801

STRAIN 2603

ATGGCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGGGACTTTTTGATACACGAGAG
CAAGCGAAACGTGGTGTTATGGCAGGAATGGTGATTAACGTTATCAATGGAGAACGTTAT
GATAAACAGGTGAAAAGGTTGCAGACGATACTGAATTAAGCTAAAAGGTGAAAACTA
AAATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCA
GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTACTGATGTTATG
CTACAATCAGGAGCGCGTTTTAGTTTACGCAGTAGATGTAGGAACAAATCAATTAGTTTGG
AAGTTACGTCAGGATCATCGTGTTCTGTTCTATGGAACAATATAATTTTAGGTATGCCCAA
AAAGAAGATTTCAAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCT
CTTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAGTAGTGGCA
TTAATTAACACCAATTTGAAGCAGGTCGTGAGCAAATTTGGTAAAAATGGTATTGTCAA
GACAAGTTGGTTTCATGAAAAGGTTTGGACAACAGTGACCAATTTACGAAAGATTATGGA
TATACGGTTAAACATCTTGATTTTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTT
TTAATGCATTTTGCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAATACAAGAT
GTTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6802

STRAIN 090

GCTAAAGAGAGGGTAGATGTTCTTGCCT
ATAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATG
GCAGGAATGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACAGG
TGAAAAGGTTGCAGACGATACTGAATTAAGCTAAAAGGTGAAAACTAA
AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTT
GAAATTTAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG
TAGATGTAGGAACAAATCAATTAGTTTGAAGTTACGTCAGGATCATCGT
GTTCTGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAGAGATTT
CAAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTC
TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA
GTAGTGGCATTAAATTAACACCAATTTGAAGCAGGTCGTGAGCAAATTTGG
TAAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAA
CAGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT
TTTTCGCCCATTTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTT

SEQUENCE LISTING

GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATG
TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6803

STRAIN A909

GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGG
CAGGAATGGTGATTAAACGTTATCAATGGAGAACGTTATGATAAACCAGGT
GAAAAGGTTGCAGACGATACTGAATTAATACTAAAAGGTGAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCAAGTTGCAGATAAGCTAATATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAAATCAATTAGTTTGAAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCCAAAAGAAGATTTT
AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCTGAGCAAATGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6804

STRAIN H36B

GCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGG
GACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGGCAGGAATG
GTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGTGAAAAGGT
TGACAGACGATACTGAATTAATACTAAAAGGTGAAAACTAAAATATGTTA
GTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCA
GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTAC
TGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGTAGATGTAG
GAACAAATCAATTAGTTTGAAGTTACGTCAGGATCATCGTGTTCGTTCT
ATGGAACAATATAATTTTAGGTATGCCCCAAAAGAAGATTTCAAGGAGGG
ACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCTTAATTTGA
TTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAGTAGTGGCA
TTAATTAACCACAATTTGAAGCAGGTCTGAGCAAATTTGGTAAAAATGG
TATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAACAGTGACCA
ATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATTTTTCGCCC
ATTCAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTGCAAAAGTG
TCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGTTATAGAAA
AAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6805

STRAIN 18RS21

GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGG
CAGGAATGGTGATTAAACGTTATCAATGGAGAACGTTATGATAAACCAGGT
GAAAAGGTTGCAGACGATACTGAATTAATACTAAAAGGTGAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCAAGTTGCAGATAAGCTAATATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGAAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGGAACAATATAATTTTAGGTATGCCCCAAAAGAAGATTT
AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCTGAGCAAATGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6806

SEQUENCE LISTING

STRAIN M732

GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGG
CAGGACTGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGC
GAAAAGGTTGCAGACGATACTGAATTAAGCTAAAGGTGAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTTCAAGTTGCAGATAAGCTAATATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGAAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCCAAAAGAAGATTTT
AAGGAGGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCCGTTCAAGGTGGACATGGAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6807

STRAIN COH1

GCTAAAGAGAGGGTAGATGTTCTTGCCT
ATAAACAGGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTATG
GCAGGACTGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGG
CGAAAAGGTTGCAGACGATACTGAATTAAGCTAAAGGTGAAAACTAA
AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTT
GAAATTTTCAAGTTGCAGATAAGCTAATATAGATATTGGCGCCTCTACGGG
TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTAGTTTACGCAG
TAGATGTAGGAACAAATCAATTAGTTTGAAGTTACGTCAGGATCATCGT
GTTTCGTTCTATGGAACAATATAATTTTAGGTATGCCCCAAAAGAAGATTT
CAAGGAGGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTC
TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA
GTAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATGG
TAAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAA
CAGTGACCAATTTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT
TTTTTCGCCCCGTTCAAGGTGGACATGGAATATTGAGTTTTTAATGCATTT
GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATG
TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6808

STRAIN M781

GCTAAAGAGAGGGTAGATGTTCTTGCCT
ATAAACAGGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTATG
GCAGGACTGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGG
CGAAAAGGTTGCAGACGATACTGAATTAAGCTAAAGGTGAAAACTAA
AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTT
GAAATTTTCAAGTTGCAGATAAGCTAATATAGATATTGGCGCCTCTACGGG
TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTAGTTTACGCAG
TAGATGTAGGAACAAATCAATTAGTTTGAAGTTACGTCAGGATCATCGT
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CAAGGAGGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTC
TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA
GTAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATGG
TAAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAA
CAGTGACCAATTTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT
TTTTTCGCCCCGTTCAAGGTGGACATGGAATATTGAGTTTTTAATGCATTT
GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATG
TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6809

STRAIN CJB110

GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGG
CAGGAATGGTGATTAACGTTATCAATGGAGAACGTTATGATAAACCAGGT

SEQUENCE LISTING

GAAAAGGTTGCAGACGATACTGAATTA AAACTAAAAGGTGAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
 AGATGTAGGAACAAATCAATTAGTTTGGAGGTTACGTCAGGATCATCGTG
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCAAAAAGAAGATTTT
 AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
 AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTGCGCCCATTCAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
 CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6810

STRAIN 1169NT

GCTAAAGAGAGGGTAGATGTTCTTGCCTA
 TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGG
 CAGGACTGGTGATTAAACGTTATCAATGGAGAACGTTATGATAAACCAGGC
 GAAAAGGTTGCAGACGATACTGAATTA AAACTAAAAGGTGAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
 AGATGTAGGAACAAATCAATTAGTTTGGAGGTTACGTCAGGATCATCGTG
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCAAAAAGAAGATTTT
 AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
 TAATTTGATTTTGCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
 AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTGCGCCCATTCAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
 CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6811

STRAIN JM9130013

GCTAAAGAGAGGGTAGATGTTCTTGCCTA
 TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGG
 CAGGAATGGTGATTAAACGTTATCAATGGAGAACGTTATGATAAACCAGGT
 GAAAAGGTTGCAGACGATACTGAATTA AAACTAAAAGGTGAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
 AGATGTAGGAACAAATCAATTAGTTTGGAGGTTACGTCAGGATCATCGTG
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCAAAAAGAAGATTTT
 AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
 AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTGCGCCCATTCAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTG
 CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6812

STRAIN 2603 frame: 1

MAKERVVDVLAYKQGLFDTRREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLE
 YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGNTQLVWK
 LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
 MHLQKQDQPNLVLDDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6813

SEQUENCE LISTING

STRAIN 090 frame: 1

AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLG
 YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
 LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6814

STRAIN A909 frame: 1

AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLG
 YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
 LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6815

STRAIN 18RS21 frame: 1

AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLG
 YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
 LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6816

STRAIN M732 frame: 1

AKERVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG
 YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
 LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6817

STRAIN COH1 frame: 1

AKERVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG
 YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
 LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6818

STRAIN M781 frame: 1

AKERVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG
 YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
 LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6819

STRAIN CJB110 frame: 1

AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLG
 YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
 LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6820

STRAIN 1169NT frame: 1

AKERVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG
 YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
 LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6821

SEQUENCE LISTING

STRAIN JM9130013 frame: 1

AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLEK
 YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
 LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6822

STRAIN H36B frame: 1

AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLEK
 YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
 LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6901

STRAIN 2603

ATGAATAAAAAGGTACTATTGACATCGACAATGGCAGCTTCGCTATTATCAGTCGCAAGT
 GTTCAAGCACAAGAAACAGATACGACGTGGACAGCAGTACTGTTTCAGAGGTAAAGGCT
 GATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACACTAAGC
 GTTATTTTCAGAAGCAATGTCATATTGATATGAATGTCTTAGCAAAAATAAATAACATTGCA
 GATATCAATCTTATTTATCCTGAGACAACACTGACAGTAACTTACGATCAGAAGAGTCAT
 ACTGCCACTTCAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCT
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 ATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCAATGAAGACATAT
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 AACCCTATGACCACGTTACGTATCATTTAACAAATAATATAAAAAAGGAAGCTATTTG
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SEQ ID NO. 6902

STRAIN 090

TGAGACAACACTGACAGTAACTTACGATCAGAAGAGTCATACTGCCACTT
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 ACTGTGGATTTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAGTTTC
 TCTCAATACAATTTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTG
 TTTTCGCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAA
 GTATTAGCACAAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGT
 ATCAACAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAG
 AGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCA
 CCAGCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACC
 GGTAAAGAACTGTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTC
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 CCTGTGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGA
 AGTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAG
 CACAACCAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCA
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 GTAAAGGTTTAGCAGTCGACTTTATTGTAGGTAAAAACCAAGCACTTGGT
 AATGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAATAACATTTTC
 ATATGTTATCTGGCAACAAAAGTTTACTCAAATACAAATAGTATTTATG
 GACCTGCTAATACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCC
 AACCATTATGACCATGTTACGTATCATTTAACAAATAATATAAAAAAGG

SEQUENCE LISTING

AAGCTATTTGGCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGTTCT
TATATAATTTTTATTA

SEQ ID NO. 6903

STRAIN A909

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAA
ATATGGTGATACACTAAGCGTTATTTTTCAGAAGCAATGTCAATTGATATGA
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AATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAaCAGcTA
CTGTCTGATTTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAGTTTCT
CTCAATACAATTTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGT
TTCCGCCAATGAAGACATATTCTTcTGCGCCAGCTTTGAAATCAAAAGAAG
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GGAGTTAATGAATTcAGTACATACCGTGCGGGAGATCCAGGTGATCATGG
TAAAGGTTTAGCAGTTGACTTTATTTGTAgGTAAaACCAAGCACTTGGTA
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ACcTGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCGTTAcTGCCA
ACCaCTATGACCAGGTTACGTATCATTTAACAAATaATATAAAAAGGA
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ATATAATTTTTATTA

SEQ ID NO. 6904

STRAIN H3B6

CTGATTTGGTAAAGCAAGACAATAAATCATCATATAcTGTGAAATA
TGCTGATACAcTAAGCGTTATTTTTCAGAAGCAATGTCaATTGATATGAATG
TCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCcTGAG
ACAACaCTGaCAGTAaCTTACGATCAGAAGAGTCATACTGCTACTTCAAT
GAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGTACTG
TCGATTTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAGTTTCTCTC
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GCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTAT
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CCAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAGGA
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CTTcTGTGTCGGCTGAAACACCAGCTCCAGTAGcTAAAGTAGCACCGGTA
AGAACTGTAGCAGCCCcTAGAGTGGCAAGTGTTAAAGTAGTCACTCcTAA
AGTAGAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCCCTG
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TCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGA
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GTTATCTGGCaACAAAAGTTTACTCAAATACAAATAGTATTTATGGACC
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ACTATGACCAGGTTACGTATCATTTAACAAATAATATAAAAAGGAAGC
TATTTGGCTTCTTTTTTATATGCCTTGCATAGACtTTCAAGGTTCTTATA
TAATTTTTATTA

SEQ ID NO. 6905

STRAIN 18RS21

CTGATTTGGTAAAGCAAGACAAT

SEQUENCE LISTING

AAATCATCATATACTGTGAAATATGGTGATACAcTAAGcGTTATTTTCAGA
 AGCAATGTCAATTGATATGAATGTCTTAGCAAAAaTAAATAACATTGCAG
 ATATCAATCTTATTTATCCTGAGACAACaCTGaCAGTAACCTTACGATCAG
 AAGAGTCATACTGCCaCTTCAATGAAAATAGAAAACACCAGCAaCAAATGC
 TGCTGGTCAaACaCAGCTACTGTGGATTTGAAAACCAATCAaGTTTCTG
 TTGCAGACCAAAAAGTTTCTCTCAATACAATTTCCGGAAGGTATGACACCA
 GAAGCAGCAACACGATTGTTTCGCCAATGAAGACaTATTCTTcTGCGCC
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 GAAGTTCAGCAGCTAAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAG
 TCAGTCAACAACAGTATCACCAGCTTCTGTTGCCGCTGAAACACCAGCTC
 CAGTAGCTAAAGTAGCACCGGTAAGAAGTGTAGCAGCCCTAGAGTGGCA
 AGTGTTAAAGTAGTCACTCCTAAAGTAGAAACTGGTGTCATCACCAGAGCA
 TGTATCAGCTCCAGCAGTTCTGTGACTACGACTTCACCAGCTACAGACA
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 ACAATAATATAAAAAAGGAAGCTATTTGGCTTCTTTTTTATATGCCTTG
 AATAGACTTTCAAGGTTCTTATATAATTTTTTATTA

SEQ ID NO. 6906

STRAIN COH1

CTGATTT

GGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACAC
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 ATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAACACTGAC
 AGTAACCTTACGATCAGAAGAGTCATACTGCCACTTCAATGAAAATAGAAA
 CACCAGCAACAAATGCTGCTGGTCAAACAACAGcTACTGTGCGATTTGAAA
 ACCAATCAAGTTTTTGTTCAGACCAAAAAGTTTcTCTCAATACAATTTT
 GGAAGGTATGACACCAGaaGCAGCAACAACGATTGTTTCGCCAATGAAGA
 CaTATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGCACAAAGAG
 CAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAGCTCCTGT
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 GCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAAGTGTAGC
 AGCCCTAGAGTGGCAAGTGcTAAAGTAGTCACTCcTAAAGTAGAACTG
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 TCACCAGCTACAGACAGTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCC
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 CAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCAACCTCAT
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SEQ ID NO. 6907

STRAIN M732

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGT
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 AGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAA
 CACTGACAGTAACCTACGATCAGAAGAGTCaTACTGCCACTTCAATGAAA
 ATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTGCA
 TTTGAAAACCAATCAAGTTTTTGTTCAGACCAAAAAGTTTCTCTCAATA

SEQUENCE LISTING

CAATTTCCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCA
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 TACGACTTCACCAGCTACAGACAGTAAGTTACAAGCGACTGAAGTTAAGA
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 TTTTATTA

SEQ ID NO. 6908

STRAIN M781

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 CACTGACAGTAACCTACGATCAGAAGAGTCATACTGCCACTTCAATGAAA
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 TTTGAAAACCAATCAAGTTTTTGTGTCAGACCAAAAAGTTTCTCTCAATA
 CAATTTCCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCA
 ATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGC
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 TCTGGCAACAAAAGTTTATTCAAATACAAATAGTATTTATGGACCTGCT
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 TTTTATTA

SEQ ID NO. 6909

STRAIN CJB110

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAA
 TATGGTGATACACTAAGCGTTATTTTCAAGCAATGTCAATTGATATGAA
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 AGCAACACTGACAGTAACCTACGATCAGAAGAGTCATACTGCCACTTCA
 ATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACACCAGCTAC
 TGTGGATTTGAAAACCAATCAAGTTTcTGTGTCAGACCAAAAAGTTTCTC
 TCAATACAATTTCCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTT
 TCCGCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGT
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 CAACAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCAGCAGCTAAAGAG
 GAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCACC
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SEQUENCE LISTING

TAAGAACTGTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCCT
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 GCTATTTGGCTTCTTTTTATATGCCTTGAATAGACtTTCAAGGTTCTTA
 TATAATTTTTATTA

SEQ ID NO. 6910

STRAIN 1169NT

CTGATTTG

GTAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACACT
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 GCCCCAGCCCCCTAGAGTGGCAAGTGCTAAAGTAGTCACTCCTAAAGTAGA
 AAcTGGTGCATCACCAGAGCATGTACCAGCTCCAGCAGTTcCTGTGACTA
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 GAATTCAGTACATaCCGTGCGGGAGATCCAGGTGATCATGGTAAAGGTTT
 AGCAGTTGACTTTATTGTAgGTAAAAACCAAGCACTTGGTAATGAAGTTG
 CACAGTACTCTACACAAAATATGGCAGCAAATAACATTTTCATATGTTATC
 TGGCAACAAAAGTTTTACTCAAATACAAATAGTATTTATGGACCTGCTAA
 TACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTATG
 ACCACGTTACGTATCATTTAACAAATAATATAAAAAAGGAAGCTATTTG
 GCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGtTCTTATATAATTT
 TTATTA

SEQ ID NO. 6911

STRAIN JM9130013

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACT

GTGAAATATGGTGATACACTAAGCGTTATTTTCAAGCAATGTCAATTGA
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 ATCCTGAGACAACACTGACAGTAACTTACGATCAGAAGAGTCATACTGCC
 ACTTCAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAAC
 AGCTACTGTGGATTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAG
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 ACTCCTAAAGTAGAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGC
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 GTAGCaCAACCAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAA

SEQUENCE LISTING

TGCAGGGCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAA
 CTTATGGAGTTAATGAATTCAGTACATACCGTGC GGGAGATCCA_gGTGAT
 CATGGTAAAGGTTTAGCAGTTGACTTTATTGTAGGTACTAATCAAGCACT
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 TATGGACCTGCTAATACTTGGAATGCAATGCCAGATCGTGGTGGCGTTAC
 TGCCAACCACTATGACCACGTTACGTATCATTTAACAAATAATATAAAA
 AAGGAAGCTATTTGGCTTCTTTTTATATGCCTTGAATAGACTTTC AAGG
 TTCTTATATAATTTTTATTA

SEQ ID NO. 6912

STRAIN 2603 frame: 1

MNKKVLLTSTMAASLLSVASVQAQETDTTWTARTVSEVKADLVKQDNKSSYTVKYGDTLS
 VISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSHTATSMKIETPATNAAGQTTA
 TVDLKTNQVSVADQKVS LNTISEGMTPEAATTIVSPMKTYSSAPALKSKEVLQEQAVSQ
 AAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVSPASVAAETPAPVAKVAPVRT
 VAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSPATDSKLQATEVKSVPVAQKAPTA
 TPVAQPASTTNAVA AHPENAGLQPHVAAYKEKVASTYGVNEFSTYRAGDPGDHGKGLAVD
 FIVGTNQALGNKVAQYSTQNMAANNISYVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTA
 NHYDHVHVSFNK.YKKGSYLASF_{LYAL}NRLSRFLY_{NFY}

SEQ ID NO. 6913

STRAIN 090 frame: 2

ETTLTVTYDQKSHTATSMKIETPATNAAGQTPATVDLKTNQVSVADQKVS LNTISEGMTP
 EAATTIVSPMKTYSSAPALKSKEVLQEQAVSQAAANEQVSTAPVKSITSEVPAAKEEVK
 PTQTSVSQSTTVSPASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVS
 PAVPVTTTSTATDSKLQATEVKSVPVAQKAPTATPVAQPASTTNAVA AHPENAGLQPHVA
 AYKEKVASTYGVNEFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNIS
 YVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASF_{LYAL}
 NRLSRFLY_{NFY}

SEQ ID NO. 6914

STRAIN A909 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
 TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVS LNTISEGMTPEAATTIVSPMKTY
 SSAPALKSKEVLQEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
 PASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSTATD
 SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVA AHPENARLQPHVAAYKEKVASTYGVN
 EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
 SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASF_{LYAL}HRLSRFLY_{NFY}

SEQ ID NO. 6915

STRAIN H36B frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
 TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVS LNTISEGMTPEAATTIVSPMKTY
 SSAPALKSKEVLQEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
 PASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSTATD
 SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVA AHPENARLQPHVAAYKEKVASTYGVN
 EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
 SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASF_{LYAL}HRLSRFLY_{NFY}

SEQ ID NO. 6916

STRAIN 18RS21 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
 TATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVS LNTISEGMTPEAATTIVSPMKTY
 SSAPALKSKEVLQEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
 PASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSPATD
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SEQ ID NO. 6917

STRAIN M732 frame: 3

DLVKQDNKSSYTVKYGDTXSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH

SEQUENCE LISTING

TATSMKIETPATNAAGQTTATVDLKTNQVFVADQKVS LNTISEGMTPEAATTIVSPMKTY
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 PASVAAETPAPVAKVAPVRTVAAPRVASAKVVT PKVETGASPEHVSAPAVPVTTTSPATD
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 EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
 SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK. YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6918

STRAIN COH1 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNV LAKINNIADINLIYPETTLTVTYDQKSH
 TATSMKIETPATNAAGQTTATVDLKTNQVFVADQKVS LNTISEGMTPEAATTIVSPMKTY
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 SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK. YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6919

STRAIN M781 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNV LAKINNIADINLIYPETTLTVTYDQKSH
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 SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK. YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6920

STRAIN CJB110 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNV LAKINNIADINLIYPETTLTVTYDQKSH
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 SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK. YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6921

STRAIN 1169NT frame: 3

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 TNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK. YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6922

STRAIN JM9130013 frame: 3

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SEQ ID. NO. 7001

STRAIN 2603

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SEQUENCE LISTING

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SEQUENCE LISTING

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SEQ ID. NO. 7002

STRAIN H36B

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SEQUENCE LISTING

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SEQ ID. NO. 7003

STRAIN 18RS21

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SEQUENCE LISTING

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 GAAATGAGGTCATCATTAAACCCAGATGTGTTGACCAACAAGTCAATGAT
 ACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTGAGTACAGTTTTGG
 TTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTGAGTCG
 GAACCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAG

SEQ ID. NO. 7004

STRAIN H36B frame: 1

GGKMNQEVLLQMMRATIPDRALLEAFLLYYQAEHFDEEWDSLIHQFMTNRQEINKSVQVL
 HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPEKNLVIEVALFNLATRFQ
 LLDSNGHYQTISPDSLLQKSRGANLVNVYRVANNLADRI SRDIEQFLTYEPELETRADE
 TVLENEETVDEHKT SVHQAI SFREEGSLVIASLDVDLSQLDVQIGKTS HLPAYEELSLRR
 KFEILTYFDQIRNERSKVP SFRRGDFDTEMEMTPVF DGEELLTYLEADGSPYELKRTLTT
 VEEKELEKIGQAIRIENQEKLTLXLSQFDPDRVGILLXAAGRXLXNADLASLGYP
 KASVTQLALATELLQMGLSHEKVEFFFGSLSIEELRQVAYAF LHQELSREDAEQFEKDK
 GNQPDLLRLDWKSKLEKAEGKEVDEEFAENPLVQRVLD TYPLGSLVSYKGQDFEVM SVS
 DARLNGLIRIELVND FSDIIEQNPLYVRTWEEVSQALHQPKAE PQTELEEADQELN LFS
 FLEEELVQSIGLLEPDDSENGHNDTLEETDNQIPEEEVVETIPEIPVTD FYPEDLTD F
 YPKTARDKVETNIVAIRLVKNLEVEHRNASPSEQELLAKYVGWGLANEFFDDYNPKFSK
 EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERD GFTGGKILDPSMG TGNEF
 AAMPKHLREKSELYGVELDTITGAIKHLHPNSHIEIKGFETVAFNDNSFDLVISNVPFA
 NIRIADNRYDRPYMIHDYFVKKSLDLLHDGGQVAIISSTGTMDKR TENILQDIRETTEFL
 GGVRLPDSAFKAIAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLN P YFDG
 EYNSQVLGTYEVRNFNGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVIINPDV LTK

SEQUENCE LISTING

QVNDTSIPAEMRENLGQYSFGYQGSTVYYRDNKGIRVGTKTEEISYYVDEE

SEQ ID. NO. 7005

STRAIN 18RS21 frame: 1

XGKMNQEVLLQMMRATIPRDRALLEAFLLYYQAEHFDEEWDLSLIHQFMTNRQEIINKSVQVL
 HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGQLQKLDKLSPEKNLVIEVALFNLATRFQ
 LLDSNGHYQTISPDSLLQKSRGANLVNVYRVANNLADRISRDI EQFLTYEPELETRADE
 TVLENEETVDEHKTSVHQAISFREEGSLVIASLDVDLSQLDVQIGKTSHLPAYEELSLRR
 KFEILTYFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEELLTYLEADGSPYELKRTLTT
 VEEKELEKIGQAIRIENQEKLTQLGIDLSQFDPDRVGILLDAAGRFRKLNADLALLGGYP
 KASVTQLALATELLQMGLSHEKVEFFFGSQLSIEELRQVAYAFHQELSREDAEQFEKDK
 GNQPDLTLRDWKSKLEKAEGKEVVDEEFAENPLVQRVLDITYPLGSLVSYKGQDFEVMVS
 DARLNGLIRIELVND FSDIIEQNPLYVVRTWEEVSQALHQPKAEPQTELEADQELNLF
 FLEEEPVQSIGLLEPDDSENGHNDTLEETDNQIP EEEVVETIPEIPVTDIFYFPEDLTD
 YPKTARDKVETNIVAIRLVKNLEVEHRNASPSEQELLAKYVGWGGLANEFFDDYNPKFSK
 EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPSMGTGNFF
 AAMPKHLREKSELYGVELDTITGAIKHLHPNSHIEIKGFETVAFNDNSFDLVISNVFPA
 NIRIADNRYDRPYMIHDFVKKSLDLLHDGGQVAIISSTGTMDKR TENILQDIRETTEFL
 GGVRLPDSAFKAIAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNYPYFDG
 EYNSQVLGTIYEVNRNFGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVIINPDVLT
 KQVNDTSIPAEMRENLGQYSFGYQGSTVYYRDNKGIRVGTKTEEISYYVDEE

SEQ ID. NO. 7006

STRAIN 2603 frame: 1

GGKMNQEVLLQMMRATIPRDRALLEAFLLYYQAEHFDEEWDLSLIHQFMTNRQEIINKSVQVL
 HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGQLQKLDKLSPEKNLVIEVALFNLATRFQ
 LLDSNGHYQTISPDSLLQKSRGANLVNVYRVANNLADRISRDI EQFLTYEPELETRADE
 TVLENEETVDEHKTSVHQAISFREEGSLVIASLDVDLSQLDVQIGKTSHLPAYEELSLRR
 KFEILTYFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEELLTYLEADGSPYELKRTLTT
 VEEKELEKIGQAIRIENQEKLTQLGIDLSQFDPDRVGILLDAAGRFRKLNADLALLGGYP
 KASVTQLALATELLQMGLSHEKVEFFFGSQLSIEELRQVAYAFHQELSREDAEQFEKDK
 GNQPDLTLRDWKSKLEKAEGKEVVDEEFAENPLVQRVLDITYPLGSLVSYKGQDFEVMVS
 DARLNGLIRIELVND FSDIIEQNPLYVVRTWEEVSQALHQPKAEPQTELEADQELNLF
 FLEEEPVQSIGLLEPDDSENGHNDTLEETDNQIP EEEVVETIPEIPVTDIFYFPEDLTD
 YPKTARDKVETNIVAIRLVKNLEVEHRNASPSEQELLAKYVGWGGLANEFFDDYNPKFSK
 EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPSMGTGNFF
 AAMPKHLREKSELYGVELDTITGAIKHLHPNSHIEIKGFETVAFNDNSFDLVISNVFPA
 NIRIADNRYDRPYMIHDFVKKSLDLLHDGGQVAIISSTGTMDKR TENILQDIRETTEFL
 GGVRLPDSAFKAIAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNYPYFDG
 EYNSQVLGTIYEVNRNFGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVIINPDVLT
 KQVNDTSIPAEMRENLGQYSFGYQGSTVYYRDNKGIRVGTKTEEISYYVDEE

SEQ ID NO. 7101

STRAIN 2603

ATGAAAAAGAAAAATTATTTTGAAGTAGTGTTCTTGGTTAGTCGCTGGGACTTCTATT
 ATGTTCTCAAGCGTGTTCGCGGACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTT
 CATGGTGCACTTGACAATACTGGAACAGCAAATATGCCTGATGGAAGTTGCTAATGCT
 GGTAAGTGTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAAACAACT
 AACCTAATGGTGAAAGCATTAGGGTCAAGCAGGCGATATGGTTGGAGCAAGTCCAGCC
 AACTCTGGGCTTCTTCAAGATGAACCAACTGTCAAAAATTTTAATGCAATGAATGTTGAG
 TATGGCACATTGGGTAACCATGAATTTGATGAAGGGTTGGCAGAATATAATCGTATCGTT
 ACTGGTAAAGCCCTGCTCCAGATTCTAATATTAATAATATTACGAAATCATACCCACAT
 GAAGCTGCAAAACAAGAAATTGTAGTGGCAAATGTTATTGATAAAGTTAACAAACAAATT
 CCTTACAATTGGAAGCCTTACGCTATTAATAATATTCTGTAAATAACAAAAGTGTGAAC
 GTTGGCTTTTACGGGATTGTCAACCAAGACATCCCAAACCTTGTCTTACGTAAAAATAT
 GAACAATATGAATTTTATAGTGAAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAA
 GCTAAAAATGTCAAGCTATTGTAGTTCTCGCACATGTACCTGCAACAAGTAAAAATGAT
 ATTGCTGAAGGTGAAGCAGAGAAATGATGAAAAAGTCAATCAACTCTTCCCTGAAAT
 AGCGTAGATATTGTTTGTCTGGACACAATCATCAATATACAAATGGTCTTGTGGTAAA
 ACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAGCCTATGCTGATGTACGTGGTGTCTTA
 GATACTGATACACAAGATTTTATTGAGACCCCTTACGCTAAAGTAATTGCAGTTGCTCCT
 GGTAAAAAACAGGTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTT
 AAACAAGTAACAGAAGCTAAAATTTGTTACTGCCGAGGTAAGTGTGATGATTACGCGTTCT
 GTTGATCAAGATAATGTAGTCCGGTAGGCAGCCTCATCACAGAGGCTCAACTAGCAATT

SEQUENCE LISTING

GCTCGAAAAAGCTGGCCAGATATCGATTTTGCCATGACAAATAATGGTGGCATTCTGTGCT
 GACTTACTCATCAAACCAGATGGAAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCT
 TTTGGTAATATCTTACAAGTCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAAC
 GAACAATACGACCAAAAACAAAATTTCTTCTTCAAATAGCTGGTCTGCGATACACTTAC
 ACAGATAATAAAGAGGGCGGGGAAGAAACACCATTAAAGTTGTAAAAGCTTATAAATCA
 AATGGTGAGGAAATCAATCCTGATGCAAAATACAAATTAGTTATCAATGACTTTTTATTC
 GGTGGTGGTGATGGCTTTGCAAGCTTCAGAAATGCCAAACTTCTAGGAGCCATTAAACCC
 GATACAGAGGTATTTATGGCTTATCTACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGC
 GTTCCAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTAAATGAACTATTACA
 CAAAATGATGGTACACATAGCATTATTAAGAACTTTATTTAGATCGACAAGGAAATAT
 GTAGCACAAGAGATTGTATCAGACACTTTAAACCAACAAAATCAAATCTACAAAAATC
 AACCTGTAACTACAATTACAAAAACAATTACACCAATTTACAGCTATTAAACCTATG
 AGAAATTATGGCAAAACCATCAAACCTCCACTACTGTAAAATCAAACAAATTACCAAAAA
 AACTCTGAATATGGACAATCATTCCTTATGTCTGTCTTTGGTGTGGACTTATAGGAATT
 GCTTTAAATACAAAGAAAAACATATGAAA

SEQ ID NO. 7102

STRAIN 090

AAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACTTGAC
 AATACTGGAACAGCAAATATGCCTGACGGAAAAAGTTACTAATGCTGGCAC
 TGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAAC
 AAACCTAACCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATGGTT
 GGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTAA
 AACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAAT
 TTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCT
 GCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGAAGC
 TGCAAAACAAGAAATTTAGTGGCAAACGTTATTGATAAAGTTAACAAC
 AAATCCCTTACAATTGGAAACCTTACGCTATTAATAAATATTCTGTAAAT
 AACAAAAGTGTAACGTTGGCTTTATCGGAATCGTTACCAAAGACATCCC
 AAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTATAGATGAAG
 CTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCAAG
 GCTATTGTAGTCCTTGGCTCATGTACCTGCAACAAGCAAGGATGATATTGC
 TGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTG
 AAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAAT
 GGTCTTGTGGTAAAACCTCGCATTGTACAAGCGCTCTCTCAAGGAAAAGC
 CTATGCTGACGTACGTGGTGTCTAGATAGTATGATACACAAGATTTTATTG
 AAACCCCTTCAGCTAAAGTAGTTGCAGTTGCTCCTGGTAAAAAACAGGT
 AGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAACA
 AGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAAGTGGCATGATTACGC
 GTTCTGTTGATCAAGATAATGTTAGTCCAGTAGGCAGCCTCATCACAGAG
 GCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGGCAT
 GACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAACCAGATGGAA
 CAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTTA
 CAAGTCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGAACA
 ATACGACCAAAAACAAAATTTCTTCTTCAAATAGCTGGTCTGCGATACA
 CTTACACAGATAATAAAGAGGGCGGAGAAGAAACACCATTAAAGTTGTA
 AAAGCTTATAAATCAAATGGTGAAGAAATCAATCCTGATGCAAAATACAA
 ATTAGTTATCAATGACTTTTTATTTCGGTGGTGGTGATGGCTTTGCAAGCT
 TCAGAAATGCCAAACTTCTAGGAGCCATTAAATCCCGATACAGAGGTATTT
 ATGGCCTATATCACTGATTTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTCC
 AAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTAAATGAACTA
 TTACACAAAATGATGGTACACATAGCATTATTAAGAACTTTATTTAGAT
 CGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACCA
 AACAAAATCAAATCTACAAAAATCAACCTGTAACTACAATTACAAAA
 AACAAATTACACCAATTTACAGCTATTAACCCCTATGAGAAATTATGGCAAA
 CCATCAAACCTCCACTACTGTAAAATCAAACAA

SEQ ID NO. 7103

STRAIN A909

GCGTCAATGACTTTTCATGGTGCACTTGACAATACTGGAACAGCAAATATG
 CCTGACGGAAAAGTTACTAATGCTGGCACTGCTGCTCAATTAGATGCTTA
 TATGGATGATGCTCAAAAAGATTTCAAACAACTAACCCCTAATGGTGAAA
 GCATTAGAGTTCAAGCTGGTGATATGGTTGGAGCAAGTCCAGCTAACTCA
 GGGCTTCTTCAAGATGAACCAACCGTTAAACATTTAATGCAATGAATGT

SEQUENCE LISTING

TGAGTATGGCACATTAGGTAACCATGAATTTGATGAAGGTTTGGCAGAAT
 ACAATCGTATCGTTACTGGAAAGGCCCTGCTCCaGaTTCTAATATAAAT
 AATATTACGAAATCATACCCACACGAAGCTGCAAAACAAGAAATTTGTAGT
 GGCAAACGTTATTGATAAAGTTAACAAACAAATCCCTTACAATTGGAAAC
 CTTACACTATTAATAAATATTCTGTAAATAACAAAAGTGTGAACGTTGGC
 TTTATCGGAATCGTTACCAAAGACATCCCAAACCTTGTCTTACGTAAAAA
 TTATGAACAATATGAATTTTTAGATGAAGCTGAAACAATCGTTAAATACG
 CCAAAGAATTACAAGCTAAAAATGTCAAGGCTATTGTAGTCCTTGCTCAT
 GTACCTGCAACAAGCAAGGATGATATTGCTGAAGGTGAAGCAGCAGAAAT
 GATGAAAAAAGTCAATCAACTCTTCCCTGAAAATAGCGTAGATATTGTCT
 TTGCTGGACACAATCATCAATATACAAATGGTCTTGTGGTAAAACTCGT
 ATTTGTACAAGCGCTCTCTCAAGGAAAAGCCTATGCTGATGTACGTGGTGT
 CCTAGATACTGATACACAAGATTTTCATTGAAACCCCTTCAGCTAAAGTAA
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 TACTGCCGAGGTAAAGTGGCATGATTACGCGTTCTGTTGATCAAGATAATG
 TTAGTCCGGTAGGCAGCCTCATCACAGAGGCTCACTAGCAATTGCTCGA
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 TGCTGACTTACTCATCAAAACCAGATGGAACAATCACCTGGGGAGCTGCAC
 AAGCAGTTCAACCTTTTGGTAATATCTTACAAGTCGTGCAAAATTAAGTGT
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 CTTCTTCAAATAGCTGGTCTGCGATACACTTACACAGATAATAAAGAGG
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 GAGGAAATCAATCCTGATGCAAAATACAAATTAGTTATCAATGACTTTTT
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 GAGCCATTAATCCCGATACAGAGGTATTTATGGCCTATATCACTGATTTA
 GAAAAAGCTGGTAAAAAAGTGAGCGTTCCAAATAATAAACCTAAAATCTA
 TGTCACTATGAAGATGGTTAATGAACTATTACACAAATGATGGTACAT
 ATAGCATTATTAAGAACTTTATTTAGATCGACAAGGAAATATTGTAGCA
 CAAGAGATTGTATCAGACACTTTAAACCAACAAAATCAAAATCTACAAA
 AATCAACCCTGTAACTACAATTACAAAAAACAAATTACACCAATTTACAG
 CTATTAACCCTATGAGAAATTATGGCAAACCATCAAACCTCCACTACTGTA
 AAATCAAAACAA

SEQ ID NO. 7104

STRAIN H36B

CCAAGTCGGTGTCGAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTTG
 ACAATACTGGAACAGCAAATATGCCTGACGGAAGTTACTAATGCTGGC
 ACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAA
 ACAAACTAACCTTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATGG
 TTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTT
 AAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGA
 ATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAGGCC
 CTGCTCCAGATTTCTAATATAAATAATATTACGAAATCATACCCACAGGAA
 GCTGCAAAACAAGAAATTTAGTGGCAAACGTTATTGATAAAGTTAACAA
 ACAATCCCTTACAATTGGAAACCTTACACTATTAATAAATATTCCTGTAA
 ATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATC
 CCAAACCTTGCTTACGTAAAAATATGAACAATATGAATTTTTAGATGA
 AGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCA
 AGGCTATTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATGATATT
 GCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTTTCCC
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 GCCTATGCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTTCAT
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 GTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAA
 CAGTAACAGAAGCTAAAATTTGGTACTGCCGAGGTAAAGTGGCATGATTAC
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 AGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCC
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 AACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCT
 TACAAGTCGTGAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGAA
 CAATACGACCAAAAAACAAATTTCTTCTTCAAATAGCTGGTCTGCGATA
 CACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTG

SEQUENCE LISTING

TAAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATAC
AAATTAGTTATCAATGACTTTTTATTTCGGTGGTGGTGATGGCTTTGCAAG
CTTCAGAAATGCCAACTTCTAGGAGCCATTAATCCCGATACAGAGGTAT
TTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAGTGAGCGTT
CCAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAAC
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CAAACAAAATCAAATCTACAAAATCAACCCTGTAACACTACAATTCACAA
AAAAAATTACACCAATTTACAGCTATTAACCCTATGAGAAATTATGGCA
AACCATCAAACCTCCACTACTGTAAAATCAAA

SEQ ID NO. 7105

STRAIN 18RS21

GACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTC
ATGGTGCACTTGACAATACTGGAACAGCAAATATGCCTGACGGAAGGTT
AnTAATGCTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCA
AAAAGATTTCAAACAACTAACCTAATGGTGAAAGCATTAGAGTTCAAG
CTGGTGATATGGTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGAT
GAACCAACCGTTAAAAACATTTAATGCAATGAATGTTGAGTATGGCACATT
AGGTAACCATGAATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTA
CTGGAAAGGCCCCCTGCTCCAGATTCTAATATAAATAATATTACGAAATCA
TACCCACACGAAGCTGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGA
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ACCAAAGACATCCCAAACCTTGTCTTACGTAAAAATTATGAACAATATGA
ATTTTGTAGATGAAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAG
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ATCAATATACAAATGGTCTTGTGGTAAAACCTCGTATTGTACAAGCGCTC
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AAAGTGAGCGTTCCAAATAATAAACCTAAAATCTATGTCACTATGAAGAT
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AACTTTATTTAGATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCA
GACACTTTAAACCAAAACAAAATCAAATCTACAAAATCAACCCTGTAAC
TACAATTCACAAAAACAATTACACCAATTTACAGCTATTAACCCTATGA
GAAATTATGGCAAACCATCAAACCTCCACTACTGTAAAATCAAAA

SEQ ID NO. 7106

STRAIN M732

ACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACCT
GACAATACTGGAACAGCAAATATGCCTGACGGAAGGTTACTAATGCTGG
CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCA
AACAACTAACCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATG
GTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGT
TAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATG
AATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAGGCC
CCTGCTCCAGATTCCTAATATAAATAATATTACGAAATCATACCCACACGA
AGCTGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTTAACA
AACAAATCCCTTACAATTGGAACCTTACACTATTAAAAATATTCTCTGTA

SEQUENCE LISTING

AATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACAT
CCCAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTGTAGATG
AAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTC
AAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATAT
TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCC
CTGAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACA
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GGTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAA
ACAAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTA
CGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
GAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGC
CATGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAACCAGATG
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ACACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTT
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CAAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGATGGCTTTGCAA
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TCCAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAA
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GATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAA
GCAAAACAAAATCAAATCTACAAAAATCAACCCTGTAACCTACAATTACA
AAAAACAATTACACCAATTTACAGCTATTAACCCCTATGAGAAATTATGGC
AAACCATCAAACCTCACTACTGTAAAATCAAAACAA

SEQ ID NO. 7107

STRAIN COH1

ACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACTT
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AACAAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATG
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TAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATG
AATTTGATGAAGGTTTGGCAGATACAATCGTATCGTTACTGGAAGGCC
CCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGA
AGCTGCAAAACAGAAATTTAGTAGTGGCAAACGTTATTGATAAAGTTAACA
AACAAATCCCTTACAATTGGAAACCTTACACTATTAAAAATATTCTCTGTA
AATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACAT
CCCAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTGTAGATG
AAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTC
AAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATAT
TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCC
CTGAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACA
AATGGTCTTGTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAA
AGCCTATGCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTCA
TTGAAACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAACA
GGTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAA
ACAAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTA
CGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
GAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGC
CATGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAACCAGATG
GAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATC
TTACAAGTCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGA
ACAATACGACCAAAAAACAAAATTCTTCTTCAAATAGCTGGTCTGCGAT
ACACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTT
GTAAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAATA
CAAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGATGGCTTTGCAA
GCTTCAGAAATGCCAACTTCTAGGAGCCATTAATCCCGATACAGAGGTA
TTTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCAT
TCCAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAA

SEQUENCE LISTING

CTATTACACAAAATGATGGTACATATAGCATTATTAAGAACTTTATTTA
 GATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAA
 CCAAAACAAAATCAAAATCTACAAAATCAACCCTGTAACCTACAAATCACA
 AAAACAATTACACCAATTTACAGCTATTAACCCCTATGAGAAATTATGGC
 AAACCATCAAACCTCCACTACTGTAAATCAAA

SEQ ID NO. 7108

STRAIN M781

CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCCTTGA
 CAATACTGGAACAGCAAATATGCCTGACGGAAGTTACTAATGCTGGCA
 CTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAA
 CAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATGGT
 TGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACGTTA
 AAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAA
 TTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAGGCCCC
 TGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGAAG
 CTGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTTAACAAA
 CAAATCCCTTACAATTGGAACCTTACACTATTAAAAATATTCCTGTAAA
 TAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACATCC
 CAAACCTTGTCTTACGTAAAAATTATGAACAAATATGAATTTTGTAGATGAA
 GCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCAA
 GGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATATTG
 CTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCCT
 GAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAA
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 GAAACCCCTTCAAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAACAGG
 TAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAAC
 AAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTACG
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 GGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
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 ACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTT
 ACAAGTCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGAAC
 AATACGACCACAAAACAAAATTTCTTCTTCAAATAGCTGGTCTGCGATAC
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 AAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATACA
 AATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGGTGGCTTTGCAAGC
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 TATGGCCTATATCACTGATTAGAAAAAGCTGGTAAAAAAGTGAGCATTC
 CAAATAATAAACCTAAAATCTATGTCACATGAAGATGGTTAATGAAACT
 ATTACACAAAATGATGGTACATATAGCATTATTAAGAACTTTATTTAGA
 TCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACC
 AAACAAAATCAAATCTACAAAATCAACCCTGTAACCTACAATTACAAA
 AAACAATTACACCAATTTACAGCTATTAACCCCTATGAGAAATTATGGCAA
 ACCATCAAACCTCCACTACTGTAAATCAAA

SEQ ID NO. 7109

STRAIN CJB110

GACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGC
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 CTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGAT
 TTCAAACAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGA
 TATGGTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAA
 CCGTTAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAAC
 CATGAATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAG
 GGCCCCCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCAC
 ACGAAGCTGCAAAACAAGAAATGTAGTGGCAAACGTTATTGATAAAGTT
 AACAAACAAATCCCTTACAATTGGAACCTTACGCTATTAAAAATATTCC
 TGTAATAAACAAGGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAG
 ACATCCCAAACCTTGTCTTACGTAAAAATTTATGAACAATATGAATTTTGA
 GATGAAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAA
 TGTCAGGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATG
 ATATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTC

SEQUENCE LISTING

TTCCCTGAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATA
TACAAATGGTCTTGTGGTAAAACCTCGCATTTGTACAAGCGCTCTCTCAAG
GAAAAGCCTATGCTGACGTACGTGGTGTCTAGATACTGATACACAAGAT
TTCATTGAAACCCCTTCAGCTAAAGTAGTTGCAGTTGCTCCTGGTAAAAA
AACAGGTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCG
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CACAGAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATT
TTGCCATGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAACCA
GATGGAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAA
TATCTTACAAGTCGTGCAAAATTACTGGTAGAGATCTTTATAAAGCACTCA
ACGAACAATACGACCAAAAACAAAATTTCTTCTTCAAATAGCTGGTCTG
CGATACACTTACACAGATAAATAAGAGGGCGGAGAAGAAACACCATTAA
AGTTGTAAAAGCTTATAAATCAAATGGTGAAGAAATCAATCCTGATGCAA
AATACAAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTATGGCTTT
GCAAGCTTCAGAAATGCCAACTTCTAGGAGCCATTAAATCCCGATACAGA
GGTATTTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGA
GCGTTCCAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAAT
GAACTATTACACAAAATGATGGTACACATAGCATTATTAAGAACTTTA
TTTAGATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTT
TAAACCAACAAAATCAAATCTACAAAATCAACCCTGTAACCTACAATT
CACAAAAAACAAATTACACCAATTACAGCTATTAACCCCTATGAGAAATTA
TGGCAAACCATCAAACCTCACTACTGTAAATCA

SEQ ID NO. 7110

STRAIN 1169NT

CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCCTTGA
CAATACTGGAACAGCAAATATGCCTGATGGAAAAGTTGCTAATGCTGGTA
CTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAAA
CAAACCTAACCCCTAATGGTGAAGCATTAGGGTTCAAGCAGGCGATATGGT
TGGAGCAAGTCCAGCCAACTCTGGGCTTCTTCAAGATGAACCAACTGTCA
AAAATTTTAATGCAATGAATGTTGAGTATGGCACATTGGGTAAACCATGAA
TTTGATGAAGGGTTGGCAGAAATATAATCGTATCGTTACTGGTAAAGCCCC
TGCTCCAGATTCTAATATTAATAATATTACGAAATCATACCCACATGAAG
CTGCAAAAACAAGAAATTGTAGTGGCAAATGTTATTGATAAAGTTAAACAA
CAAATTCCTTACAATTGGAAGCCTTACGCTATTAAAAATATTCTGTAAA
TAACAAAAGTGTGAACGTTGGCTTTATCGGGATTGTCAACAAAGACATCC
CAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTGTAGATGAA
GCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCAA
AGCTATTGTAGTCTCGCACATGTACCTGCAACAAGTAAAAATGATATTG
CTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCT
GAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAA
TGGTCTTGTGGTAAAACCTCGTATTGTACAAGCGCTCTCTCAAGGAAAAG
CCTATGCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTCATT
GAGACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAACAGG
TAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAAC
AAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGTCTATGATTACG
CGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
GGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
TGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAACCAGATGGA
ACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTT
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AATACGACCAAAAACAAAATTTCTTCTTCAAATAGCTGGTCTGCGATAC
ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTAAAGTTGT
AAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATACA
AATTAGTTATCAATGACTTTTATTTCGGTGGTGGTATGGCTTTGCAAGC
TTCAGAAATGCCAACTTCTAGGAGCCATTAAACCCGATACAGAGGTATT
TATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTC
CAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAACT
ATTACACAAAATGATGGTACACATAGCATTATTAAGAACTTTATTTAGA
TCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACC
AAACAAAATCAAATCTACAAAATCAACCCTGTAACCTACAATTACAAA
AAACAATTACACCAATTACAGCTATTAACCCCTATGAGAAATTATGGCAA
ACCATCAAACCTCACTACTGTAAATCAAA

SEQUENCE LISTING

SEQ ID NO. 7111

STRAIN JM9130013

CGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTTGACAATA
 CTGGAACAGCAAATATGCCTGACGGAAAAGTTACTAATGCTGGCACTGCT
 GCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAACAAAC
 TAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATGGTTGGAG
 CAAGTCCAGCTAATCAGGGCTTCTTCAAGATGAACCAACCGTTAAACAA
 TTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAATTTGA
 TGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCTGCTC
 CAGATTCTAATATAAATAATATTACGAAATCATACCCACACGAAGCTGCA
 AAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTTAACAACAAAT
 CCCTTACAATTGGAACCTTACACTATTAAAAATATTCTGTAAATAACA
 AAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATCCCAAAC
 CTTGTCTTACGTAAAAATTATGAACAATATGAATTTTAGATGAAGCTGA
 AACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCAAGGCTA
 TTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATGATATTGCTGAA
 GGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTGAAAA
 TAGCGTAGATATTGCTTTGCTGGACACAATCATCAATATACAAATGGTC
 TTGTTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAGCCTAT
 GCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTTCATTGAAAC
 CCCTTCAGCTAAAGTAATTGCAAGTTGCTCCTGGTAAAAAACAGGTAGTG
 CCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAACAAGTA
 ACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTACGCGTTC
 TGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGAGGCTC
 AACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCATGACA
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 CACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTTACAAG
 TCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGAACAATAC
 GACCAAAAAACAAATTTCTTCCTTCAAATAGCTGGTCTGCGATACACTTA
 CACAGATAATAAGAGGGCGGGGAAGAAACACCATTAAAGTTGTAAG
 CTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATACAAATTA
 GTTATCAATGACTTTTTATTTCGGTGGTGGTATGGCTTTGCAAGCTTCAG
 AAATGCCAAACTTCTAGGAGCCATTATCCCGATACAGAGGTATTTATGG
 CCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTCCAAAT
 AATAAACCTAAATCTATGTCACTATGAAGATGGTTAATGAAACTATTAC
 ACAAATGATGGTACATATAGCATTATTGAGAACTTTATTAGATCGAC
 AAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACCAAACA
 AAATCAAAATCTACAAAAATCAACCTGTAACTACAATTACAAAAACA
 ATTACACCAATTTACAGCTATTAACCCCTATGAGAAATTATGGCAAACCAT
 CAAACTCCACTACTGTAAATCAAAA

SEQ ID NO. 7112

STRAIN 2603 frame: 1

MKKKIILKSSVLGLVAGTSMIFSSVFADQVGVQVIGVNDHFHGLDNTGTANMPDGKVANA
 GTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVGASPA NSGLLQDEPTVKNFNAMNVE
 YGTLGNHEFDEGLAEYNRIVTGKAPAPDSNINNITKSY PHEAAKQEI VVANVIDKVNKQI
 PYNWKPYAIKNIPVNNKSVNVGFIGIVTKDIPNLVLRKNYEQYEFLEAETIVKYAKELQ
 AKNVKAI VVLAHV PATSKNDIAEGEAAEMMKVNQLFPENSVDIVFAGHNHQYTNGLVGK
 TRIVQALSQKAYADVRGVLDTDTQDFIETPSAKVIAVAPGKKTGSADIQAI V DQANTIV
 KQVTEAKIGTAEVSMITRSVDQDNVSPVGS LITEAQLAIARKSWPDIDFAMTNNGGIRA
 DLLIKPDGTITWGAAQAVQPFGNILQVVEITGRDLYKALNEQYDQKQNF FLQIAGLRYTY
 TDNKEGGEETPFKVVKAYKSN GEEINPD AKYKLVINDFLFEGGGDGFASFRNAKLLGAINP
 DTEVF MAYITDLEKAGKKVSV PNNKPKIYVTM K MVNETITQNDGTHSIIKKLYLDRQGN I
 VAQEIVSDTLNQTKSKSTKINPVTTIHKQLHQFTAINPMRNYGKPSNSTTVKSKQLPKT
 NSEYGQSFLMSVFGVGLIGIALNTKKKHKM

SEQ ID NO. 7113

STRAIN 090 frame: 3

VGQVIGVNDHFHGLDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRV
 QAGDMVGASPA NSGLLQDEPTVKTFNAMNVEYGT LGNHEFDEGLAEYNRIVTGKAPAPDS
 NINNITKSY PHEAAKQEI VVANVIDKVNKQI PYNWKPYAIKNIPVNNKSVNVGFIGIVTK
 DIPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAEM
 MKKNVQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQKAYADVRGVLDTDTQDFIE

SEQUENCE LISTING

TPSAKVAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPV
 GSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVVE
 ITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNNGEINPDA
 KYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPKIY
 VTMKMNVTITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTHKK
 QLHQFTAINPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7114

STRAIN A909 frame: 3

VNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVG
 ASPANSGLLQDEPTVKTFFNAMNVEYGT LGNHEFDEGLAEYNRIVTGKAPAPDSNNITK
 SYPHEAAKQEIIVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIVTKDIPNLVL
 RKNYEQYEFLEAETIVKYAKELQAKNVKAIVVLAHV PATSKDDIAEGEAAEMMKVNQL
 FPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADV RGVLD TDTQDFIETPSAKVI
 AVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPV GSLITEA
 QLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVVEITGRDLY
 KALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNNGEINPDAKYKLVIN
 DFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPKIYV TMKMN
 VTITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTHKKQLHQFTA
 INPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7115

STRAIN H36B frame: 2

QVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGAS PANSGLLQDEPTVKTFFNAMNVEYGT LGNHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSY PHEAAKQEIIVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIVT
 KDIPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAIVVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADV RGVLD TDTQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 V GSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQV
 VEITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNNGEINP
 DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPKI
 YVTMKNVTITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7116

STRAIN 18RS21 frame: 1

DQVGVQVIGVNDFHGALDNTGTANMPDGKVXNAGTAAQLDAYMDDAQKDFKQTNPNGESI
 RVQAGDMVGAS PANSGLLQDEPTVKTFFNAMNVEYGT LGNHEFDEGLAEYNRIVTGKAPAP
 DSNINNITKSY PHEAAKQEIIVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIV
 TKDIPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAIVVLAHV PATSKDDIAEGEAA
 EMMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADV RGVLD TDTQDF
 IETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVS
 PV GSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQV
 VEITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNNGEINP
 DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPKI
 IYVTMKNVTITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTH
 KQLHQFTAINPMRNYGKPSNSTTVKSK

SEQ ID NO. 7117

STRAIN M732 frame: 3

QVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGAS PANSGLLQDEPTVKTFFNAMNVEYGT LGNHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSY PHEAAKQEIIVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIVT
 KDIPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAIVVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADV RGVLD TDTQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 V GSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQV
 VEITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNNGEINP
 DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPKI
 YVTMKNVTITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTHK
 KQLHQFTAINPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7118

SEQUENCE LISTING

STRAIN COH1 frame: 3

QVGQVIGVNDFFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEIIVANVIDKVNKQIPYNWKPYTIKNI PVNNKSVNVGFIGIVT
 KDIPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAIVVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQ GKAYADVRGVLD TDTQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVV KAYKSN GEEINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVF MAYITDLEKAGKKVSI PNNKPKI
 YVTMKNVNETITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7119

STRAIN M781 frame: 1

QVGQVIGVNDFFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEIIVANVIDKVNKQIPYNWKPYTIKNI PVNNKSVNVGFIGIVT
 KDIPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAIVVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQ GKAYADVRGVLD TDTQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVV KAYKSN GEEINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVF MAYITDLEKAGKKVSI PNNKPKI
 YVTMKNVNETITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7120

STRAIN CJB110 frame: 1

DQVGQVIGVNDFFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESI
 RVQAGDMVGASPANSGLLQDEPTVKTFFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAP
 DSNINNITKSYPHAAKQEIIVANVIDKVNKQIPYNWKPYAIKNI PVNNKSVNVGFIGIV
 TKDIPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAIVVLAHV PATSKDDIAEGEAA
 EMMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQ GKAYADVRGVLD TDTQDFI
 IETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 PVGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQV
 VETITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVV KAYKSN GEEINP
 DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVF MAYITDLEKAGKKVSV PNNKPK
 IYVTMKNVNETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7121

STRAIN 1169NT frame: 1

QVGQVIGVNDFFHGALDNTGTANMPDGKVANAGTAAQLDAYMDDAQKDFKQTNPNGESIR
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 SNINNITKSYPHAAKQEIIVANVIDKVNKQIPYNWKPYAIKNI PVNNKSVNVGFIGIVT
 KDIPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAIVVLAHV PATSKNDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQ GKAYADVRGVLD TDTQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSVMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVV KAYKSN GEEINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVF MAYITDLEKAGKKVSV PNNKPKI
 YVTMKNVNETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
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SEQ ID NO. 7122

STRAIN JM9130013 frame: 2

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 INNITKSYPHAAKQEIIVANVIDKVNKQIPYNWKPYTIKNI PVNNKSVNVGFIGIVTKD
 IPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAIVVLAHV PATSKDDIAEGEAAEMM
 KKNVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQ GKAYADVRGVLD TDTQDFIET
 PSAKVIAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPVG
 SLITEAQLAIARKSWPDI DFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVVEI

SEQUENCE LISTING

TGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVVKAYKSNNGEEINPDAK
YKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSVNNKPKIYV
TMKMNNETITQNDGTYSIIIEKLYLDRQGNIVAQEIIVSDTLNQTKSKSTKINPVTIHKKQ
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SEQ ID NO. 7201

STRAIN 2603

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TTAACTGGGGTGTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTTG
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SEQ ID NO. 7202

STRAIN 090

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SEQUENCE LISTING

TGCAGAACGTGTAGCACTTGAAGCAGGACTTGTGAATCAGGCGATAATA
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SEQ ID NO. 7203

STRAIN A909

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SEQ ID NO. 7204

STRAIN H36B

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SEQUENCE LISTING

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SEQ ID NO. 7205

STRAIN 18RS21

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SEQ ID NO. 7206

STRAIN M732

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SEQUENCE LISTING

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SEQ ID NO. 7207

STRAIN COH1

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SEQ ID NO. 7208

STRAIN M781

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SEQUENCE LISTING

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SEQ ID NO. 7209

STRAIN CJB110

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SEQ ID NO. 7210

STRAIN 1169NT

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SEQUENCE LISTING

CCTTTCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTTGGACT
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 AAGTTGTTTGTcTAAATTTGAAAATCAaCAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGTGAAATGGTTCAGTTTACCAAAAaAATGATCATTACT
 AaAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACACGTCGCGACTCGTTCAGAAGTATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAACATtACTCAATGAGTATGGTCGTTTAGACTCATCTG
 CATTCCACGTAATTAACAAAACCTGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACCTGTTGTGAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTATTGATGATTAACCTGGGGT
 GTTATCCCTGTCCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
 GGTTCGAGAACGTGTAGCACTTGAAGCAGGACTTGTGAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCCCTGTAGGTACAGGTGGAACAAACACA
 ATGCGTGTTTCGTACTGTTAAA

SEQ ID NO. 7211

STRAIN JM9130013

AATAAACGCGTAAAAATCGTTGCAAC

ACTTGGTCCTGCGGTAGAATTCGGTGGTAAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAGGTGCTAACGTTTTCCGTTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
 ATTCGTACAGAACTTTTGAAGATGGTTCAGATTCCATTTCATATACAAC
 AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
 CCTTTCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACTTTATTGCTATCTCATTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACATGTT
 AAGTTGTTTGCTAAAATTGaAAATCAaCAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTAttACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACACGTCGCGACTCGTTCAGAAGTATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCCACGTAATAaCAAACTGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACCTGTTGTGACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTATTGATGATTAACCTGGGGT
 GTTATCCCTGTCCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
 GGTTCGAGAACGTGTAgcACTTGAAGCAGGACTTGTGAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCCCTGTAGGTACAGGTGGAACAAACACA
 ATGCGTGTTTCGTACTGTTAAA

SEQ ID NO. 7212

STRAIN 2603 frame: 1

MNKRKIVATLGPVFRGGKKGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHG
 DHAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQ
 GIKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLI
 GKQKGVNIPYTKIPFPALAEARNADIRFGLQGLNFIAISFVRTAKDVNEVRAICEETGX
 GHVKLFAKIENQQGIDNIDEIIEADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGK
 AVITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVTRMATID
 KNAQILLNEYGRLDSSAFPRNKTDVIASAVKDATHSMDIKLVVTTITETGNTARAIKFR
 PDADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVI

SEQUENCE LISTING

VAGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7213

STRAIN 090 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEIAGQKVGFLDDTKGPEIRTELFEDGSDHSTTTGTCLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLENEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
 DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7214

STRAIN A909 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEIAGQKVGFLDDTKGPEIRTELFEDGADHSTTTGTCLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLENEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
 DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7215

STRAIN H36B frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEIAGQKVGFLDDTKGPEIRTELFEDGADHSTTTGTCLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLENEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
 DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7216

STRAIN 18RS21 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEIAGQKVGFLDDTKGPEIRTELFEDGADHSTTTGTCLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLENEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
 DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7217

STRAIN M732 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEIAGQKVGFLDDTKGPEIRTELFEDGADHSTTTGTCLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLENEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
 DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7218

STRAIN COH1 frame: 1

SEQUENCE LISTING

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRNFSHGD
 HAEQGARMATVRKAEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVENDGLIG
 KQKGVNIPYTKIPFPALAEARNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIASAVKDATHSMDIKLVTTITETGNTARAIKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7219

STRAIN M781 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRNFSHGD
 HAEQGARMATVRKAEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVENDGLIG
 KQKGVNIPYTKIPFPALAEARNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIASAVKDATHSMDIKLVTTITETGNTARAIKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7220

STRAIN CJB110 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRNFSHGD
 HAEQGARMATVRKAEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVENDGLIG
 KQKGVNIPYTKIPFPALAEARNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIASAVKDATHSMDIKLVTTITETGNTARAIKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7221

STRAIN 1169NT frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRNFSHGD
 HAEQGARMATVRKAEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVENDGLIG
 KQKGVNIPYTKIPFPALAEARNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIASAVKDATHSMDIKLVTTITETGNTARAIKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7222

STRAIN JM9130013 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRNFSHGD
 HAEQGARMATVRKAEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVENDGLIG
 KQKGVNIPYTKIPFPALAEARNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIASAVKDATHSMDIKLVTTITETGNTARAIKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7301

STRAIN 2603

TTGTCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTTAGCATTAATCGGTGAT
 ATCATTAAATTCAAAACAGATACTTGAACGTGAACTTTCCAACAGTCTTTTCAGCACTA
 ATGACCGAATCTGATGATATGTTGAAGAGCTGATTTCTCCATTCACATTACAGCT
 GGTGATGAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGACCAT

SEQUENCE LISTING

ATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCTGGCCTCGGTACAGGAAACATTATA
 ACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCCTGCCTACTGGCATGCTCGC
 TCAGCTATTAATCATATACATGATAAAAAATGATTATGGAACAGTTCAAGTAGCTATTGTC
 CTGATGATGAAGACCAAAACCTTGAATTAACACTAAATAGTCTCATTTAGCTGGTGAT
 TTTATCAAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAA
 GATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCACTGGAAAATATTGAACCT
 AGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTGAAGATTTACTTAAGAACGAGAACA
 CAGGCAGCCGATCTATTAGTTAAAAGTTGCACTCAAACCTAAAGGGGAAGCTATGATTTTC

SEQ ID NO. 7302

STRAIN 090

TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTT
 AGCATTAAATCGGTGATATCATTAATTCAAACAGATACTTGAACGTGAAA
 CTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTGATGTATAT
 GGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTTCA
 AGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTTATTGACCATATTC
 AACTAGCTCTAAAACCTGTTAATGTAAGGTTCTGGCCTCGGTACAGGAAAC
 ATTATAACATCCATCAATTTAAATGAAAGTATCGGTGCTGATGGTCCTGC
 CTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAAAAAATGATT
 ATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACCAAAACCTT
 GAATTAACACTAAATAGTCTCATTTAGCTGGTGATTTTATCAAGTCAAA
 ATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGATA
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 GAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTGAAGATTTA
 CTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAGTTGCACTC
 AAACCTAAAGGGGAAGCTATGATTTTC

SEQ ID NO. 7303

STRAIN A909

TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTAT
 TTAGCATTAAATCGGTGATATCATTAATTCAAACAGATACTTGAACGTGA
 AACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTGATGTAT
 ATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTT
 CAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTTATTGACCATAT
 TCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCTGGCCTCGGTACAGGAA
 ACATTATAACATCCATCAATTTCAAATGAAAGTATCGGTGCTGATGGTCCT
 GCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAAAAAATGA
 TTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACCAAAACC
 TTGAATTAACACTAAATAGTCTCATTTAGCTGGTGATTTTATCAAGTCA
 AAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGA
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 TTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTGAAGATT
 TACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAGTTGCAC
 TCAAACCTAAAGGGGAAGCTATGATTTTC

SEQ ID NO. 7304

STRAIN H36B

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
 ATGTATTTAGCATTAAATCGGTGATATCATTAATTCAAACAGATACTTGA
 ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTTATTGA
 CCATATTTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCTGGCCTCGGT
 CAGGAAACATTATAACATCCATCAATTTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAA
 AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC
 AAAACCTTGAATTAACACTAAATAGTCTCATTTAGCTGGTGATTTTATC
 AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAG
 TTGCACTCAAACCTAAAGGGGAAGCTATGATTTTC

SEQ ID NO. 7305

SEQUENCE LISTING

STRAIN 18RS21

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
ATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTGA
ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
GAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGA
CCATATTTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTA
CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
GGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAA
AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC
AAAACCTTGAATTAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTATC
AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
TCAAGATAATTTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
AAAATATTGAACCTAGTGCCTGACTAAACGCCTTAAAGCAAGCGGTCTG
AAGATTTACTTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
TTGCACTCAAACATAAGGGGGAAGCTATGATTTTC

SEQ ID NO. 7306

STRAIN M732

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
TATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTG
AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
TGAATTTCAAGCTTTATTGAAACaATCAAAAAAGGTATTTCAAATTATTG
ACCATATTTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGT
ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
TGGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATA
AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
CAAACCTTGAATTAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTAT
CAAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATAC
TTCAAGATAAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTG
GAAAATATTGAACCTAGTGCCTGACTAAACGCCTTAAAGCAAGCGGTCT
GAAGATTTACTTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAA
GTTGCACTCAAACATAAGGGGGAAGCTATGATTTTC

SEQ ID NO. 7307

STRAIN COH1

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
TATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTG
AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
TGAATTTCAAGCTTTATTGAAACaATCAAAAAAGGTATTTCAAATTATTG
ACCATATTTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGT
ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
TGGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATA
AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
CAAACCTTGAATTAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTAT
CAAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATAC
TTCAAGATAAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTG
GAAAATATTGAACCTAGTGCCTGACTAAACGCCTTAAAGCAAGCGGTCT
GAAGATTTACTTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAA
GTTGCACTCAAACATAAGGGGGAAGCTATGATTTTC

SEQ ID NO. 7308

STRAIN M781

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
ATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTGA
ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
GAATTTCAAGCTTTATTGAAACAATCAAAAAAGGTATTTCAAATTATTGA
CCATATTTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTA
CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
GGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAA
AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC

SEQUENCE LISTING

AAAACCTTGAATTAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTATC
 AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
 AAAATATTGAACCTAGTGGCTGACTAAACGCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAAGACGAGAACACAGGCAGCCGATCTATTAGTTAAAAG
 TTGCACTCAAACATAAGGGGGAAGCTATGATTTTc

SEQ ID NO. 7309

STRAIN CJB110

TCTGCTATAATAGACAAAAAGGTGGTGGTA
 TTTATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACT
 TGAACGTGAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAAGTAT
 CTGATGTATATGGTGAAGAGCTGATTTCTCTATTCACTATTACAGCTGGT
 GATGAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTAT
 TGACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCG
 GTACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCT
 GATGGTCCTGCCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGA
 TAAAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAG
 ACCAAAACCTTGAATTAACACTAAATAGTCTCATTTTCAGCTGGTGATTTT
 ATCAAGTCAAAATGGACTACTAACCATTTTCAAATGCTTGAGCACTTAAT
 ACTTCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAAC
 TGGAAAATATTGAACCTAGTGGCTGACTAAACGCCTTAAAGCAAGCGGT
 CTGAAGATTTACTTAAAGACGAGAACACAGGCAGCCGATCTATTAGTTAA
 AAGTTGCACTCAAACATAAGGGGGAAGCTATGATTTTc

SEQ ID NO. 7310

STRAIN JM9130013

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
 ATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTGA
 ACGTGAACCTTTCCAACAGTCTTTTCAGCAACTAATGACCGAAGTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGA
 CCAATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTA
 CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
 GGTCTCGCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAA
 AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC
 AAAACCTTGAATTAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTATC
 AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
 AAAATATTGAACCTAGTGGCTGACTAAACGCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAAGACGAGAACACAGGCAGCCGATCTATTAGTTAAAAG
 TTGCACTCAAACATAAGGGGGAAGCTATGATTTTc

SEQ ID NO. 7311

STRAIN 2603 frame: 1

LSAIDKKVVFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITA
 GDEFQALLKPSKKVFQIIDHIQLALKPVNVRFLGTGNIITSINSNESIGADGPAYWHAR
 SAINHIHDKNDYGTQVAICLDDEDQNLLELTLSLISAGDFIKSKWTTNHFQMLEHLILQ
 DNYQEQQFQHQKLAQLENIEPSALT KRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7312

STRAIN 090 frame: 1

SAIDKKVVFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFLGTGNIITSINL NESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDEDQNLLELTLSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENIEPSALT KRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7313

STRAIN A909 frame: 1

SAIDKKVVFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDEDQNLLELTLSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENIEPSALT KRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQUENCE LISTING

SEQ ID NO. 7314

STRAIN H36B frame: 1

SAIIDKKVVIIFYMLALIGDIINSKQILERETFQQS FQQLMTELS DVYGEELISPFTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTVQVAICLDDEDQNL ELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQE QFQH QKLAQLENIEPSALT KRLKASGLKIYLRTRTQAADLLVKSC TQTKGGSYDF

SEQ ID NO. 7315

STRAIN 18RS21 frame: 1

SAIIDKKVVIIFYMLALIGDIINSKQILERETFQQS FQQLMTELS DVYGEELISPFTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTVQVAICLDDEDQNL ELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQE QFQH QKLAQLENIEPSALT KRLKASGLKIYLRTRTQAADLLVKSC TQTKGGSYDF

SEQ ID NO. 7316

STRAIN M732 frame: 1

SAIIDKKVVIIFYMLALIGDIINSKQILERETFQQS FQQLMTELS DVYGEELISPFTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTVQVAICLDDEDQNL ELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQE QFQH QKLAQLENIEPSALT KRLKASGLKIYLRTRTQAADLLVKSC TQTKGGSYDF

SEQ ID NO. 7317

STRAIN COH1 frame: 1

SAIIDKKVVIIFYMLALIGDIINSKQILERETFQQS FQQLMTELS DVYGEELISPFTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTVQVAICLDDEDQNL ELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQE QFQH QKLAQLENIEPSALT KRLKASGLKIYLRTRTQAADLLVKSC TQTKGGSYDF

SEQ ID NO. 7318

STRAIN M781 frame: 1

SAIIDKKVVIIFYMLALIGDIINSKQILERETFQQS FQQLMTELS DVYGEELISPFTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTVQVAICLDDEDQNL ELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQE QFQH QKLAQLENIEPSALT KRLKASGLKIYLRTRTQAADLLVKSC TQTKGGSYDF

SEQ ID NO. 7319

STRAIN CJB110 frame: 1

SAIIDKKVVIIFYMLALIGDIINSKQILERETFQQS FQQLMTELS DVYGEELISLFTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTVQVAICLDDEDQNL ELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQE QFQH QKLAQLENIEPSALT KRLKASGLKIYLRTRTQAADLLVKSC TQTKGGSYDF

SEQ ID NO. 7320

STRAIN JM9130013 frame: 1

SAIIDKKVVIIFYMLALIGDIINSKQILERETFQQS FQQLMTELS DVYGEELISPFTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTVQVAICLDDEDQNL ELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQE QFQH QKLAQLENIEPSALT KRLKASGLKIYLRTRTQAADLLVKSC TQTKGGSYDF

SEQ ID NO. 7401

STRAIN 2603

ATGGAAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACACTCTAT
 CTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGGATTTTA
 AGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAAATACGGGACTTTTACTCAAGCAC
 TTTGATATTACTACTAAACAAATTAGTTTTACGGAACACAATGCTTACGATAAAATCTCT
 GGGTTAATTGATTTGTTAAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATG
 CCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
 GTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGGTTTAGCT
 CCACAACCTCATATTTTTTATGGCTTCTTACCTCGTAAGAAAGGTCAACAAATAACTTTC
 TTTGAAACAAAGCAAGATTACCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTC
 TCTGATACGCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGC
 GAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGAGCAT
 ATTGAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAGAGAGATACC
 GAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAGTATTAGTAAAAGAATATATCGCT

SEQUENCE LISTING

AATGGTGATAAACTAATCAAGCGATAAAAAAGTAGCAAAAGAATTTAATCTCAATAGA
CAAGAACTCTATGCTAGTTTCCATGATTTA

SEQ ID NO. 7402

STRAIN 090

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATTACGGGACACT
CTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTG
CCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGA
AATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAG
TTTTACGAACACAATGCTTACGATAAAATCTCTGGGTAAATTGATTTGT
TAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCT
ATTTCTGACCCAGgACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGA
CCCGGTGCTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCG
CTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCGCGT
AAGAAAGGTCAACAAATAACTTTTTTTGAAACAAGAAAGATTACCCTGa
AACACAAATCTTTATGAGTCACCGTTTCGAGTCTcTGATACGCTAAAC
ACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATTG
ACGAAaCTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGG
GCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATG
GTAAGAGAGATACCGAGCGAGTGAAGACAGTAGCCAACAAGATCCACTA
GTATTAGTAA

SEQ ID NO. 7403

STRAIN A909

AGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACACTCTATCTAG
TCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGG
ATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAAATACGGG
ACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAGTTTTCACG
AACACAATGCTTACGATAAAATCTCTGGGTAAATTGATTTGTTAAAAGAA
GGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATTTCTGA
CCCAGGACATGAACCTTGTCAAGGCTGCTATTGAAGGGGATATCCAGTTG
TATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGGT
TTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCACGTAAGAAAGG
TCAACAAATAACTTTCTTTgAAACAAAGCAAGATTACCCTGAAACACAAA
TCTTTTATGAGTCACCGTTTCGAGTCTCtGATACGCTAAACACATGAAA
GAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATTGACGAAACT
CTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGAGCATATTG
AAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAGAGA
GATACCGAGCGAGTGAAGACAGTAGCCAACAAGATCCACTAGTATTAGT
AA

SEQ ID NO. 7404

STRAIN H36B

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATT
ACGGGACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATG
ACTTTTCGTGCCATTAGGATTTTAAGAgAAGTTGATTTTATTTGTGCAGA
GGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTCACGAACACAATGCTTATGATAAAATCTCTGGGTAA
ATTGATTTGTTAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGG
AATGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCCGGTGCTATCTATACCAGGAGCTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTT
CTTACCGCGTAAGCAAGGTCAACAAATAACTTTTTTTGAAACAAGAAAG
ATTACCCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGAT
ACGCTAAAACACATGAAAGAGATTTATGGAGATCGCCAAGTTGTTTTAGT
ACGCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTC
AACTTTTAGGGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAGAGAGATACGTAGCGAGTGAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7405

STRAIN 18RS21

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATT
ACGGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAgATGATATG

SEQUENCE LISTING

ACTTTtCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGA
 GgATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
 AACAAATTAGTTTTTACGAACACAATGCTTACGATAAAATCTCTGGGTTA
 ATTGATTTGTTAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGG
 AATGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
 AAGGGGATATCCCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACT
 GCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTT
 CTTACCACGTAAGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAG
 ATTACCCTGAAACACAAATCTTTTTATGAGTCACCGtTTCGAGTCTCTGAT
 ACGCTAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGT
 ACGCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTC
 AACTTTTAGAGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
 ATTGTTGATGGTAAGAGAGATACCGAGCGAGTGAAGACAGTAGCCAACA
 AGATCCACTAGTATTAGTAA

SEQ ID NO. 7406

STRAIN M732

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAAT
 ATACATTACGGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGA
 TGATATGACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTT
 GTGCAGAGGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATT
 ACTACTAAACAAATTAGTTTTTACGAACACAATGCTTACGATAAAATCTC
 TGGGTTAATTGATTTGTTAAAGAAGGGAAATCTTTAGCCCAAGTATCTG
 ATGCAGGAATGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCT
 GCTATTGAAGGGGATATCCCAGTTGTATCTATACCAGGAGCTAGCGCTGG
 TATTACTGCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTT
 ATGGCTTCTTACCACGTAAGAAAGGTCAACAAATAACTTTCTTTGAAACA
 AAGCAAGATTACCTGAAACACAAATCTTTTTATGAGTCACCGtTTCGAGT
 CTCTGATACGCTAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTG
 TTTTAGTACGGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACC
 ATTAGTCAACTTTTAGAGCATATTGAAAAGGTCCCTCTCAAAGGTGAATG
 CTTAATTATTGTTGATGGTAAGAGAGATACCGAGCGAGTGAAGACAGTA
 GCCAACAAGATCCACTAGTATTAGTAA

SEQ ID NO. 7407

STRAIN COH1

GAAATGCAAGTTCAAAAAAGTTTTaAATCAAATATACATTAC
 GGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGAC
 TTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGG
 ATACACGAAATACGGGAcTTTTACTCAAGCACTTTGATATTACTACTAAA
 CAAATTAGTTTTTACGAACACAATGCTTACGATAAAATCTCTGGGTAAAT
 TGATTTGTTAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAA
 TGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAA
 GGGGATATCCCAGTTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGC
 TCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCT
 TACCACGTAAGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAGAT
 TACCCTGAAACACAAATCTTTTTATGAGTCACCGtTTCGAGTCTCTGATAC
 GCTAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTAC
 GCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAA
 CTTTTAGAGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTAT
 TGTTGATGGTAAGAGAGATACCGAGCGAGTGAAGACAGTAGCCAACAAG
 ATCCACTAGTATTAGTAA

SEQ ID NO. 7408

STRAIN M781

AAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACACTC
 TATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGC
 CATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACCGAA
 ATACGGgACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAGT
 TTTCACGAACACAATGCTTACGATAAAATCTCTGGGTAAATTGATTTGTT
 AAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTcTA
 TTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATC
 CCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGC
 TTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCACGTA

SEQUENCE LISTING

AGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAGATTACCCTGAA
 ACACAAATCTTTATGAGTCACCGTTTCGAGTcTcTGATACGCTAAAAACA
 CATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTGTAGTACGCGAATTGA
 CGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGAG
 CATATTGAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGG
 TAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAG
 TATTAGTAA
 A

SEQ ID NO. 7409

STRAIN CJB110

GAAATGCAAGTTCAAAAAGTTTAAATCAAATACACATTACGGGACAC
 TCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGT
 GCCATTAGGATTTTAAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACG
 AAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTA
 GTTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTAAATTGATTTG
 TTAAGAGAAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTC
 TATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGA
 TCCCGGTGCTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATC
 GCTTCAGGTTTAGCTCCACAACCTCATATTTTATGGCTTCTTACCGCG
 TAAGAAAGGTCAACAAATAACTTTtTTTGAACAAAGAAAGATTACCCTG
 AAACACAAATCTTTTATGAGTCACCGtTTcGAGTCTCTGATACGCTAAAA
 CACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATT
 GACGAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAG
 GGCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGAT
 GGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACT
 AGTATTAGTAA

SEQ ID NO. 7410

STRAIN 1169NT

TGCAAGTTCAAAAAGTTTAAATCAAATACACATTATGGGACACTCTAT
 CTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCAT
 TAGGATTTTAAAGAgAAGTTGaTTTTATTTGTGCAGAGGATACACGAAATA
 CGGGACTTTTACTCAAGCACTTTGATaTTACTACTAAACAAATTAGtTTT
 cACGAACACAATGCTTACGATAAAATCTCTGGGTAAATTGATTtGTTAAA
 AGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATTT
 CTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
 GTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTC
 AGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCACGTAAGA
 AAGTCAACAAATAACTTTTTTTGAAACAAAGCAAGATTATCCTGAAACA
 CAAATCTTTTATGAGTCACCGtTTcGAGTCTCTGATACGCTAAACACAT
 GAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATTGACgA
 AACTCTATGAAGAGTATCAAAGAGGAACCATTaGTCAACTTTTAGAGCAT
 ATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGtTGATGGTAA
 GAGAGAtaCCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAGTAT
 TAGTAA

SEQ ID NO. 7411

STRAIN JM9130013

GAAATGCAAGTTCAAAAAGTTTAAATCAAATACACATTACGGGA
 CACTCTATCTAGTCCCAACTCCAATTGGTAATCTAgATGATATGACTTTT
 CGTGCCATTAGGATTTTAAAGAGAAGTTGATTTTATTTGTGCAGAGGATAC
 ACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAA
 TTAGTTTTTACGAACACAATGCTTATGATAAAATCTCTGGGTAAATTGAT
 TTGTAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCC
 CTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGG
 ATATCCCGGTGCTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTC
 ATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACC
 GCGTAAGCAAGGTCAACAAATAAcTTTTTTGAAACAAAGAAAGATTACC
 CTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTA
 AAACACATGAAAGAGATTTATGGAGATCGCCAAGTTGTTTTAGTACGCGA
 ATTGACGAACTCTATGAAGAGTATCAAaGAGGAACCATTAGTCAACTTT
 TAGGGCATATTGaAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTT
 GATGGTAAGAGAGATACTGAGCGAGTGAAAGACAGTAGCCAACAAGATCC

SEQUENCE LISTING

AGTAGTATTAGTAA

SEQ ID NO. 7412

STRAIN 2603 frame: 1

MEMQVQKSFKSNIHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
DITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDIPV
VSIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVS
DTLKHMKIYGDRQVVLVRELTKLYEYQRTISQLEHIEKVPLKGECLIIVDGKRDTE
RVKDSSQQDPLVLVKEYIANGDKTNQAIKKVAKEFNLNRQELYASFHDL

SEQ ID NO. 7413

STRAIN 090 frame: 1

EMQVQKSFKSNIHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAIEGGIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKKDY PETQIFYESPFRVSD
TLKHMKIYGDRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7414

STRAIN A909 frame: 2

VQKSFKSNIHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDITT
KQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAIEGDIPVVSIP
GASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDTLK
HMKIYGDRQVVLVRELTKLYEYQRTISQLEHIEKVPLKGECLIIVDGKRDTERVKD
SSQQDPLVLV

SEQ ID NO. 7415

STRAIN H36B frame: 1

EMQVQKSFKSNIHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAIEGDIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKKDY PETQIFYESPFRVSD
TLKHMKIYGDRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7416

STRAIN 18RS21 frame: 1

EMQVQKSFKSNIHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKIYGDRQVVLVRELTKLYEYQRTISQLEHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7417

STRAIN M732 frame: 1

EMQVQKSFKSNIHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKIYGDRQVVLVRELTKLYEYQRTISQLEHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7418

STRAIN COH1 frame: 1

EMQVQKSFKSNIHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKIYGDRQVVLVRELTKLYEYQRTISQLEHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7419

STRAIN M781 frame: 3

MQVQKSFKSNIHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDI
TTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDIPVVS
IPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDT
LKHMKIYGDRQVVLVRELTKLYEYQRTISQLEHIEKVPLKGECLIIVDGKRDTERV

SEQUENCE LISTING

KDSSQQDPLVLV

SEQ ID NO. 7420

STRAIN CJB110 frame: 1

EMQVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDT
ITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPSISDPGHDLVKAIEGGIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQTFFETKKDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDTERR
VKDSSQQDPLVLV

SEQ ID NO. 7421

STRAIN 1169NT frame: 3

QVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDT
TKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPSISDPGHDLVKAIEGGIPVVS
PGASAGITALIASGLAPQPHIFYGFLPRKKGQQTFFETKKDYPETQIFYESPFRVSDTL
KHMKEIYGDRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDTERRV
DSSQQDPLVLV

SEQ ID NO. 7422

STRAIN JM9130013 frame: 1

EMQVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDT
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SEQ ID NO. 7501

STRAIN 2603

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SEQUENCE LISTING

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SEQ ID NO. 7502

STRAIN 090

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SEQ ID NO. 7503

STRAIN A909

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SEQUENCE LISTING

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SEQ ID NO. 7504

STRAIN H36B

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SEQUENCE LISTING

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SEQ ID NO. 7505

STRAIN 18RS21

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SEQ ID NO. 7506

STRAIN M732

SEQUENCE LISTING

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SEQ ID NO. 7507

STRAIN COH1

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SEQUENCE LISTING

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SEQ ID NO. 7508

STRAIN M781

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CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
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SEQUENCE LISTING

TCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAAA
CTATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTTCAGCACAAAGTCC
TCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACAA
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SEQ ID NO. 7509

STRAIN CJB110

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ATATAAAAATCAGCACTCTATTTAGAATCTTATACAGGAAGCATAACTA
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SEQ ID NO. 7510

STRAIN 1169NT

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CGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATT
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SEQUENCE LISTING

ATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATT
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SEQ ID NO. 7511

STRAIN JM9130013

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 GTGCTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAAGTA
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 TGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTCCAGAAAATT

SEQUENCE LISTING

TTGTCTATCATCAAAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTTT
 TCGTTTGCTTTTGGTGGAATAATAGTGGTGTCTTATTGTCATCTTTAGA
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 GGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7512

STRAIN 2603 frame: 1

MSVYVSGIGIISLGNKYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQ
 YKDETRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTS LGGKSAGQNALYQFEGERQV
 DASLLEKASVYHIADELMAYHDIVGASYVISTAC SASNNAVILGTQLLQDGDCLAI CGG
 CDELS DISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKY GKIIGGL
 ITSDGYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKF
 FPTTT LISSTKGQTGHTLGAAGIIE LINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKR
 EYPI RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITY
 EKVASNFNDFEALRFKARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTS
 KVGIVFTT LSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLS IIFKITGPLSV
 ISTNSGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSA
 QVLSRQALDNSPIILGSKQLKYSHKTFDVM TIFDAALQNL LSDLGLTIKDIKGFVWNER
 KKAVSSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIF
 GGISFAIEKR

SEQ ID NO. 7513

STRAIN 090 frame: 3

VSGIGIISLGNKYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTS LGGKSAGQNALYQFEGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTAC SASNNAVILGTQLLQDGDCLAI CGG CDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKY GKIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSTKGQTGHTLGAAGIIE LINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGIILLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTT LSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLS IIFKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPIILGSKQLKYSHKTFDVM TIFDAALQNL LSDLGLTIKDIKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7514

STRAIN A909 frame: 3

VSGIGIISLGNKYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTS LGGKSAGQNALYQFEGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTAC SASNNAVILGTQLLQDGDCLAI CGG CDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKY GKIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSTKGQTGHTLGAAGIIE LINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI

SEQUENCE LISTING

RNALNFSFAFGGNNSGVLLSSLDSPLETLTPARENLMKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKARPPKTVNPAQFRKMDDFSKMAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFDVTMIFDAALQNLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLAGSQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYSIFGGIS
FAIEKR

SEQ ID NO. 7515

STRAIN H36B frame: 3

VSGIGIISLGGKKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTS LGGKSAGQNALYQFEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGVLLSSLDSPLETLTPARENLMKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKARPPKTVNPAQFRKMDDFSKMAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFDVTMIFDAALQNLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLAGSQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYSIFGGIS
FAIEKR

SEQ ID NO. 7516

STRAIN 18RS21 frame: 3

VSGIGIISLGGKKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTS LGGKSAGQNALYQFEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGVLLSSLDSPLETLTPARENLMKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKARPPKTVNPAQFRKMDDFSKMAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFDVTMIFDAALQNLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLAGSQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYSIFGGIS
FAIEKR

SEQ ID NO. 7517

STRAIN M732 frame: 3

VSGIGIISLGGKKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTS LGGKSAGQNALYQFEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGVLLSSLDSPLETLTPARENLMKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKARPPKTVNPAQFRKMDDFSKMAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFDVTMIFDAALQNLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLAGSQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYSIFGGIS
FAIEKR

SEQ ID NO. 7518

STRAIN COH1 frame: 3

VSGIGIISLGGKKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTS LGGKSAGQNALYQFEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI

SEQUENCE LISTING

RNALNFSFAFGGNNSGVLLSSLDSPLETLTPARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKARPPKTVNPAQFRKMDDFSKMAVTTAQALIESNINLKKQDTSKVGI
 VFTTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPIILGSKQLKYSHKTFDVTMIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLA SQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7519

STRAIN M781 frame: 3

VSGIGIISLGGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNEKFAFTAFEEALASSGVNLKAYHNIACVCLGTS LGGKSAGQNALYQFE EGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTAC SASNNAVILGTQLLQDGD CDLAICGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFPTT
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 RNALNFSFAFGGNNSGILLSSLDSPLETLTPARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKARPPKTVNPAQFRKMDDFSKMAVTTAQALIESNINLKKQDTSKVGI
 VFTTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPIILGSKQLKYSHKTFDVTMIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLA SQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7520

STRAIN CJB110 frame: 3

VSGIGIISLGGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNEKFAFTAFEEALASSGVNLKAYHNIACVCLGTS LGGKSAGQNALYQFE EGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTAC SASNNAVILGTQLLQDGD CDLAICGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFPTT
 TLISSTKGQTGHTLGAAGIIE LINCLAAIEEQTVPATKNEIGIEGFPENFVYHQREYPI
 RNALNFSFAFGGNNSGILLSSLDSPLETLTPARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKARPPKTVNPAQFRKMDDFSKMAVTTAQALIESNINLKKQDTSKVGI
 VFTTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPIILGSKQLKYSHKTFDVTMIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLA SQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7521

STRAIN 1169NT frame: 3

VSGIGIISLGGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNEKFAFTAFEEALASSGVNLKAYHNIACVCLGTS LGGKSAGQNALYQFE EGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTAC SASNNAVILGTQLLQDGD CDLAICGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFPTT
 TLISSTKGQTGHTLGAAGIIE LINCLAAIEEQTVPATKNEIGIEGFPENFVYHQREYPI
 RNALNFSFAFGGNNSGILLSSLDSPLETLTPARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKARPPKTVNPAQFRKMDDFSKMAVTTAQALIESNINLKKQDTSKVGI
 VFTTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPIILGSKQLKYSHKTFDVTMIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLA SQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7522

STRAIN JM9130013 frame: 3

VSGIGIISLGGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNEKFAFTAFEEALASSGVNLKAYHNIACVCLGTS LGGKSAGQNALYQFE EGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTAC SASNNAVILGTQLLQDGD CDLAICGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFPTT
 TLISSTKGQTGHTLGAAGIIE LINCLAAIEEQTVPATKNEIGIEGFPENFVYHQREYPI

SEQUENCE LISTING

RNALNFSFAFGGNNSGVLLSSLDSPLETLTPARENLMKMAILSSVASISKNESLSITYEKVA
 SNENDFEALRFKGRPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTSLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSQDYCSAQVLS
 RQALDNSPIILGSKQLKYSHKFTFDVMTIFDAALQNLSDLGLTIKDIKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLSAQGFSSNGAGEELDYTVNESIEKGYLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7601

STRAIN 2603

ATGAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATATGCCTCAGAAACCGTTTTA
 AATAATATTAAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAATAGGACCCCTCGGA
 GCAGGGAATCTACCTTGATTAATACTATGCTTGGCATGGAAAAAGCAGATAAGGGAACA
 GCTCTTGTTCTTGATACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATG
 GCTCAATCTGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCTTTGGA
 AAAATGAAAGGTATTCAAAAACTGAATTAACACAGCAGATAACTCATATTTCTAAAGTA
 GTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAAAAGA
 CGGCTTTCTCTAGCCATCGCCCTACTTGGAACCCACAGTTTAAATCCTAGATGAACCT
 ACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAG
 GATGAAGGACATTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAAGT
 AAGGTTGCACTACTATTACGTGGAAACATTATGCCTTTGATACTCCATTACATTTAAAA
 AAACAATTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7602

STRAIN 090

ATTTAAAAAACTACAAAAAGCATATGCCTCAGAAACTGTTTAAATAAT
 ATTAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAATAGGACCCCTC
 TGGAGCAGGGAATCTACCTTGATTAATACTATGCTTGGCATGGAAAAAG
 CAGATAAGGGAACAGCTCTTGTTCTTGATACTCAAATGCCAGATCGTAAT
 ATTTTAAATCAAATTGGCTATATGGCTCAATCTGATGCCTTATACGAATC
 TTTAACTGCCCTTAGAAaATTATTATTCTTTGAAAAAATGAAAGGTATTCT
 AAAAACTGAATTAACACAGCAGATAACTCATATTTCTAAAGTAGTAGAT
 CTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAA
 AAGACGGCTTTCTCTAGCCATCGCCCTACTTGGAACCCACAGTTTAA
 TCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATC
 TGGCAAGAGCTAATTAATATTAaGGATGAAGGACGTTCTATCTTTATTAC
 AACCCACGTTATGGATGAAGCAGAATTAACAAGTAAGGTTGCACTACTAT
 TACGTGGAACATTATTGCCTTTGATACTCCATTACATTTAAAAAAACAA
 TTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7603

STRAIN A909

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATATGCCTCA
 GAAACCGTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAAATAAT
 TGGATTAATAGGACCCCTCTGGAGCAGGGAATCTACCTTGATTAATACTA
 TGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACT
 CAAATGCCAGATCATAATATTTTAAATCAAATTGGCTATATGGCTCAATC
 TGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCTTTG
 GAAAAATGAAAGGTATTCAAAAACTGAATTAACACAGCAGATAACTCAT
 ATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGG
 TTAATCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTG
 GAAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATTGATCCA
 TCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGAAGG
 ACGTTCTATCTTTATTATTACAAACCCACGTTATGGATGAAGCAGAATTAACA
 GTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACTCCA
 TTACATTTAAAAAAACAAATTAATGTGAGTACTATTGAGGAAGTTTCTT
 AAAAGCTGAAGGAGAA

SEQ ID NO. 7604

STRAIN H36B

AAAAAAGTCATTGATTTAAAAAACTACAAAAAGCATATGCC
 TCAGAAACCGTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAAAT
 AATTGGATTAATAGGACCCCTCTGGAGCAGGGAATCTACCTTGATTAATA
 CTATGCTTGGCATGGAAAAAGCAGATAAGGGAaCAGCTCTTGTTCTTGAT

SEQUENCE LISTING

ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCA
 ATCTGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCT
 TTGGAAAAATGAAAGGTATTCAAAAACTGAATTTAAACAGCAGATAACT
 CATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTC
 AGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTAC
 TTGGAAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGAT
 CCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGA
 AGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAA
 CAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACT
 CCATTACATTTAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTTT
 CTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7605

STRAIN 18RS21

GATTTAAAAAACTACAAAAAGCATATGCCTCAGAAACCGTTTTAAATAA
 TATTAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAATAGGACCTT
 CTGGAGCAGGGAAATCTACcTTGATTAAAACTATGCTTGGCATGGAAAAA
 GCAGATAAGGGAACAGCTCTTGTTCTTGATACTCAAATGCCAGATCGTAA
 TATTTTAAATCAAATTGGCTATATGGCTCAATcTGATGCCTTATACGAGT
 CTTTAACTGGCTTAGAAAATTTATTATTCTTTGGAAAAATGAAAGGTATT
 CAAAAAACTGAATTTAAAAACAGCAGATAACTCATATTTCTAAAGTAGTAGA
 TCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGA
 AAAGACGGCTTTCTcTAGCCATCGCCCTACTTGGAACCCACAGTTTTA
 ATCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAAT
 CTGGCAAGAGCTAATTAATATTAaGGATGAAGGACATTCTATCTTTATTA
 CAACCCACGTTATGGATGAAGCAGAATTAACAAGTAAGGTTGCACTACTA
 TTACGTGGAAACATTATTGCCTTTGATACTCCATTACATTTAAAAAACA
 ATTTAATGTGAGTACTATTGAGGAAGTTTTCTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7606

STRAIN M732

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATACGCCTCA
 GAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGAAATAAT
 TGGATTAATAGGACCTCTGGAGCAGGGAAATCTACCTTGATTAAAACTA
 TGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACT
 CAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCAATC
 TGATGCCTTACACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCTTTG
 GAAAAATGAAAGGTATTCAAAAACTGAATTTAAACAGCAGATAACTCAT
 ATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGG
 TTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTG
 GAAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCA
 TCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGAAGG
 ACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAA
 GTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACTCCA
 TTACATTTAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTTTCTT
 AAAAGCTGAAGGAGAA

SEQ ID NO. 7607

STRAIN COH1

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATACGCCTCAGAA
 ACTGTTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGAAATAATTGG
 ATTAATAGGACCTCTGGAGCAGGGAAATCTACCTTGATTAAAACTATGC
 TTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACTCAA
 ATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCAATCTGA
 TGCCTTACACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCTTTGGAA
 AAATGAAAGGTATTCAAAAACTGAATTTAAACAGCAGATAACTCATATT
 TCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTA
 CTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTGAA
 ACCCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCATCC
 TTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGAAGGACG
 TTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAAGTA
 AGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACTCCATTA
 CATTTAAAAAACAATTTAATGTGAGTACTATTGAGGAAG

SEQUENCE LISTING

SEQ ID NO. 7608

STRAIN M781

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATAC
GCCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGA
AATAATTGGATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTA
AACTATGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTT
GATACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCTTACACGAGTCTTTAACTGGCTTAGAAAATTTATTAT
TCTTTGGAAAAATGAAAGGTATTCAAAAACTGAATTTAAACAGCAGATA
ACTCATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGT
CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCC
TACTTGGAAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATT
GATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGA
TGAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
TAACAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGAT
ACTCCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGT
TTTCTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7609

STRAIN CJB110

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATATG
CCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAA
ATAATTGGATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTA
AACTATGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTG
ATACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCT
CAATCTGATGCCTTATACGAATCTTTAACTGCCTTAGAAAATTTATTATT
CTTTGGAAAAATGAAAGGTATTCAAAAACTGAATTTAAACAGCAGATAA
CTCATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTC
TCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCT
ACTTGGAAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTG
ATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGAT
GAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATT
AACAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATA
CTCCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTT
TTCTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7610

STRAIN 1169NT

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATAC
GCCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGA
AATAATTGGATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTA
AACTATGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTT
GATACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCTTATACGAATCTTTAACTGCCTTAGAAAATTTATTAT
TCTTTGGAAAAATGAAAGGTATTCAAAAACTGAATTTAAACAGCAGATA
ACTCATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGT
CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCC
TACTTGGAAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATT
GATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGA
TGAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
TAACAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGAT
ACTCCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGT
TTTCTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7611

STRAIN JM9130013

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATATGCC
TCAGAAACCGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAAAT
AATTGGATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTA
CTATGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGAT
ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCA
ATCTGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCT
TTGGAAAAATGAAAGGTATTCAAAAACTGAATTTAAACAGCAGATAACT
CATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTC

SEQUENCE LISTING

AGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTAC
 TTGGAAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATTGAT
 CCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGA
 AGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAA
 CAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTCCTTTGATACT
 CCATTACATTTAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTT
 CTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7612

STRAIN 2603 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTA
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRLSLAIALLGNTPTVLILDEPTVGIDPSLRKRWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPHLKKQFNV

SEQ ID NO. 7613

STRAIN 090 frame: 3

LKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTA
 QMPDRNINLQIGYMAQSDALYESLTGLENLFFGKMKGIQKTELKQQITHISKVV
 LDKEFVSGYSGGMKRRLSLAIALLGNTPTVLILDEPTVGIDPSLRKRWQELINIKDEGRSI
 FITTHVMDEAELTSKVALLLRGNIIAFDTPHLKKQFNV

SEQ ID NO. 7614

STRAIN A909 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTA
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRLSLAIALLGNTPTVLILDEPTVGIDPSLRKRWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPHLKKQFNV

SEQ ID NO. 7615

STRAIN H36B frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTA
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRLSLAIALLGNTPTVLILDEPTVGIDPSLRKRWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPHLKKQFNV

SEQ ID NO. 7616

STRAIN 18RS21 frame: 1

DLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTA
 TQMPDRNINLQIGYMAQSDALYESLTGLENLFFGKMKGIQKTELKQQITHISKVV
 QLDKFVSGYSGGMKRRLSLAIALLGNTPTVLILDEPTVGIDPSLRKRWQELINIKDEGHS
 IFITTHVMDEAELTSKVALLLRGNIIAFDTPHLKKQFNV

SEQ ID NO. 7617

STRAIN M732 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTA
 LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRLSLAIALLGNTPTVLILDEPTVGIDPSLRKRWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPHLKKQFNV

SEQ ID NO. 7618

STRAIN COH1 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTA
 LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRLSLAIALLGNTPTVLILDEPTVGIDPSLRKRWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPHLKKQFNV

SEQ ID NO. 7619

STRAIN M781 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTA
 LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRLSLAIALLGNTPTVLILDEPTVGIDPSLRKRWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPHLKKQFNV

SEQUENCE LISTING

SEQ ID NO. 7620

STRAIN CJB110 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTM LGMEKADKGTA
 LVLDQTQMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKG IQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRRLSLAIALLLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPHLHLKKQFNV

SEQ ID NO. 7621

STRAIN 1169NT frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTM LGMEKADKGTA
 LVLDQTQMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKG IQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRRLSLAIALLLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPHLHLKKQFNV

SEQ ID NO. 7622

STRAIN JM9130013 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTM LGMEKADKGTA
 LVLDQTQMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKG IQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRRLSLAIALLLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPHLHLKKQFNV

SEQ ID NO. 7701

STRAIN 2603

TTGCCATGTTGCTGTTGGTTTTAGTTTTAGAGGGTGGCGGAATGAGAGGTCTTTATACT
 GCTGGAGTTTTAGATGCTTTTCTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTC
 TCTGCTGGTGCAATTTGTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
 TACAATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGTTTTCGAACA
 GGGAAATTTTGTAAATAAAGATTTTACCTATTATGAAGTTCCTATGAAATTGGATGTATTT
 GACGATGAAGCATTTAAAAAATCAAGTATTGATTTTTACGTAGTTGCTACAGAGATGACA
 TCTGGTAAACCTGAATATTTTAAATTTGATAGTGTTTTTGAACAAATGGAAATTTTACGT
 GCTAGTTGAGCATTTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
 GATGGTGGTTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGATTTGACAAG
 TTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCCTTCAAGTGGACGATTG
 TATAAACTCTGTATAGGAAATATCCTAATTTTGTAAAGACAGCCTCGAATCGGTACCAA
 CAGTATAATAATAGTCTTGAAAAGTCTGAGCCTTGAAAAAACAGGCGATCTATTTGCA
 ATTAGACCGAGTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
 AGTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAATAGTTAT
 CTAATGAAA

SEQ ID NO. 7702

STRAIN 090

CCTATGTTGCTGTTGGTTTTAGTTTTAG
 AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTT
 CTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGCTCTGCTGGTGC
 ATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
 ACAATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGG
 TTTCGAACAGGGAAATTTTGTAAATAAAGATTTTACCTATTATGAAGTTC
 TATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
 ATTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
 AAAATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGC
 ATTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
 ATGGTGGTTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTAGGA
 TTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAA
 GCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATT
 TTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAA
 AAGGTCATGAGCCTTGAAAAACAGGCGATCTATTGCAATTAGACCGAG
 TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
 GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTG
 AATAGTTATCTAATGAAA

SEQ ID NO. 7703

STRAIN A909

CCTATGTTGCTGTTGGTTTTAGTTTTAGAG
 GGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTTCT

SEQUENCE LISTING

AGATGCAGGAATAAAAGTAGATGGTATCATATCTGTCTCTGCTGGTGCAT
TGTTTGGTGTAAATTTGTATCTAGACAACGAGAGAGGGCTTTGCGATAC
AATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGCT
TCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTA
TGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGAT
TTTTACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTTAA
AATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGCAT
TACCAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
GGTGGTTTATCTGATAGTATTCCTGTTGATTTTGCCCGTGGTTTAGGATT
TGACAAGTTGATTGTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGC
CTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTT
GTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAAAA
GGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCAAGTA
AGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGT
ATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTGAA
TAGTTATCTAATGAAA

SEQ ID NO. 7704

STRAIN H36B

CCTATGTTGTCTGTTGGTTTAGTTTTAG
AGGGTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTTAGATGCTTTT
CTAGATGCAGGAATAAAAGTAGATGGTATCATATCTGTCTCTGCTGGTGC
ATTGTTTGGTGTAAATTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGG
CTTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTC
TATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
ATTTTTACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTT
AAAATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGC
ATTACCAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTCCTGTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
GCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATT
TTGTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAA
AAGGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCAAG
TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTG
AATAGTTATCTAATGAAA

SEQ ID NO. 7705

STRAIN 18RS21

CCTATGTTGTCTGTTGGTTTAGTTTTAGAGG
GTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTTAGATGCTTTTCTA
GATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCTGGTGCATT
GTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATACA
ATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGTTT
CGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTAT
GAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGATT
TTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAA
ATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGCATT
ACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATG
GTGGTTTATCTGATAGTATTCCTGTTGATTTTGCCCGTGGTTTAGGATT
GACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCC
TTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTTG
TAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAAAG
GTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCGAGTAA
GAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGTA
TTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAAT
AGTTATCTAATGAAA

SEQ ID NO. 7706

STRAIN M732

CCTATGTTGTCTGTTGGTTTAGTTTTAGA
GGGTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTTAGATGCTTTTC
TAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCA

SEQUENCE LISTING

TTGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATA
CAATAAAAAGTATTTATCCCACCCTGAATATATGAGTCTAAGATCATGGC
TTCGAACAGGGAATTTTGTAAATAAAGATTTCACCTATTATGAAGTTCCT
ATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGA
TTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTA
AAATTGATAGTGTATTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGCA
TTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGA
TGGTGGTTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGAT
TTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAG
CCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTT
TGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAA
AGGTCATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGAGT
AAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAG
TATTTATCAGCTTGGTATGAAATATGCTAAAAGTGTGATGCCTGAGCTGA
ATAGTTATCTAATGAAA

SEQ ID NO. 7707

STRAIN COH1

CCTATGTTGTCTGTTGGTTTAGTTTTA
GAGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTT
TCTAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTG
CATTGTTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
TACAATAAAAAGTATTTATCCCACCCTGAATATATGAGTCTAAGATCATG
GCTTCGAACAGGGAATTTTGTAAATAAAGATTTCACCTATTATGAAGTTC
CTATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATT
GATTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
TAAATTGATAGTGTATTTTGAACAAATGGAAATTTTACGTGCTAGTTCAG
CATTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
GATGGTGGTTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGG
ATTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
AGCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
TTTGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
AAAGGTCATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGA
GTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
AGTATTTATCAGCTTGGTATGAAATATGCTAAAAGTGTGATGCCTGAGCT
GAATAGTTATCTAATGAAA

SEQ ID NO. 7708

STRAIN M781

CCTATGTTGTCTGTTGGTTTAGTTTTAG
AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTT
CTAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGC
ATTGTTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAGTATTTATCCCACCCTGAATATATGAGTCTAAGATCATGG
CTTCGAACAGGGAATTTTGTAAATAAAGATTTCACCTATTATGAAGTTC
TATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
ATTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
AAAATTGATAGTGTATTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGC
ATTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
GCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATT
TTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAA
AAGGTCATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGAG
TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAATATGCTAAAAGTGTGATGCCTGAGCTG
AATAGTTATCTAATGAAA

SEQ ID NO. 7709

STRAIN CJB110

CCTATGTTGTCTGTTGGTTTAGTTTTA
GAGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTT
TCTAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCTGGTG
CATTGTTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA

SEQUENCE LISTING

TACAATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATG
GTTTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTC
CTATGAAATTTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATT
GATTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
TAAAATTGATAGTGTATTTTGAACAAATGGAAATTTACGTGCTAGTTCAG
CATTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
GATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTAGG
ATTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
AGCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
TTTGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
AAAGGTCATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGA
GTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
AGTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCT
GAATAGTTATCTAATGAAA

SEQ ID NO. 7710

STRAIN 1169NT

CCTATGTTGTCTGTTGGTTTGTAGTTTGTAGAGGGTG
GCGGAATGAGAGGTCTTTTACTGCTGGAGTTTGTAGATGCTTTTCTAGAT
GCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCATTGTT
TGGTGTAAATTTGTATCTAGACAACGAGAGAGGGCTTTGCGATACAATA
AAAAGTATTTTATCCCACCCTAAATATATGAGTCTAAGATCATGGCTTCGA
ACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTATGAA
ATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGATTTTT
ACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAATTT
GATAGTGTCTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGCATTACC
AGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATGGTG
GTTTATCTGATAGTATCCCCGTTGATTTTGCCCGTGGTTTAGGATTGAC
AAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCCTTC
AAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTGTAA
AGACAGCCTCGAATCGGTACCAACAGTATAATAATAGCCTTGAAAAGGTC
ATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGGCCGAGTAAAAG
CTTGGTTATTGTCCGCTTAGAGAAGAATCCGGATAAACTTGATAGTATTT
ATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAATAGT
TATCTAATGAAA

SEQ ID NO. 7711

STRAIN JM9130013

CCTATGTTGTCTGTTGGTTTGTAGTTTGTAGAG
GGTGGCGGAATGAGAGGTCTTTTACTGCTGGAGTTTGTAGATGCTTTTCT
AGATGCAGGAATAAAGTAGATGGTATCATATCTGTCTCTGCTGGTGCAT
TGTTTGGTGTAAATTTGTATCTAGACAACGAGAGAGGGCTTTGCGATAC
AATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGCT
TCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTA
TGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGAT
TTTTACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTTAA
AATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGCAT
TACCAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
GGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGATT
TGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGC
CTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTT
GTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAAAA
GGTCATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCAAGTA
AGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGT
ATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTGAA
TAGTTATCTAATGAAA

SEQ ID NO. 7712

STRAIN 2603 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKYLSHPKYMSLRSWFRTGNFVNKDFTYEVPKMLDVFDDFAFKKSSIDFYVVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTASNRYQQYNNLSLEKVMSEKLTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPELNSYLMK

SEQUENCE LISTING

SEQ ID NO. 7713

STRAIN 090 frame: 1

PMLSVGLVLEGGGMRGLYTAGVLD AFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYL SHPKYMSLR SWFRTGNFVNKDFTYE VPMKLDVFDDEAFKKSSIDFYV VATEMTS
GKPEYFKIDS VFEEQMEIL RASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVM SLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPELNSYLMK

SEQ ID NO. 7714

STRAIN A909 frame: 1

PMLSVGLVLEGGGMRGLYTAGVLD AFLDAGIKVDGII SVSAGALFGVNFVSRQRERALRY
NKKYL SHPKYMSLR SWLRTGNFVNKDFTYE VPMKLDVFDDEAFKKSSIDFYV VATEMTS
GKPEYFKIDS VFEEQMEIL RASSALPVVSKMVVWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVM SLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7715

STRAIN H36B frame: 1

PMLSVGLVLEGGGMRGLYTAGVLD AFLDAGIKVDGII SVSAGALFGVNFVSRQRERALRY
NKKYL SHPKYMSLR SWLRTGNFVNKDFTYE VPMKLDVFDDEAFKKSSIDFYV VATEMTS
GKPEYFKIDS VFEEQMEIL RASSALPVVSKMVVWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVM SLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7716

STRAIN 18RS21 frame: 1

PMLSVGLVLEGGGMRGLYTAGVLD AFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYL SHPKYMSLR SWFRTGNFVNKDFTYE VPMKLDVFDDEAFKKSSIDFYV VATEMTS
GKPEYFKIDS VFEEQMEIL RASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVM SLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPELNSYLMK

SEQ ID NO. 7717

STRAIN M732 frame: 1

PMLSVGLVLEGGGMRGLYTAGVLD AFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYL SHPEYMSLR SWLRTGNFVNKDFTYE VPMKLDVFDDEAFKKSSIDFYV VATEMTS
GKPEYFKIDS VFEEQMEIL RASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVM SLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKYAKSVMPELNSYLMK

SEQ ID NO. 7718

STRAIN COH1 frame: 1

PMLSVGLVLEGGGMRGLYTAGVLD AFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYL SHPEYMSLR SWLRTGNFVNKDFTYE VPMKLDVFDDEAFKKSSIDFYV VATEMTS
GKPEYFKIDS VFEEQMEIL RASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVM SLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKYAKSVMPELNSYLMK

SEQ ID NO. 7719

STRAIN M781 frame: 1

PMLSVGLVLEGGGMRGLYTAGVLD AFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYL SHPEYMSLR SWLRTGNFVNKDFTYE VPMKLDVFDDEAFKKSSIDFYV VATEMTS
GKPEYFKIDS VFEEQMEIL RASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVM SLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKYAKSVMPELNSYLMK

SEQ ID NO. 7720

STRAIN CJB110 frame: 1

PMLSVGLVLEGGGMRGLYTAGVLD AFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYL SHPKYMSLR SWFRTGNFVNKDFTYE VPMKLDVFDDEAFKKSSIDFYV VATEMTS
GKPEYFKIDS VFEEQMEIL RASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVM SLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPELNSYLMK

SEQUENCE LISTING

SEQ ID NO. 7721

STRAIN JM9130013 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGIISVSAGALFGVNFVSRQRERALRY
 NKLYLSHPKYMSLRSLWRTGNFVNKDFYYEVPKLDVDFDEAFKKSSIDFYAVATEMTS
 GKPEYFKIDSVEFQMEILRASSALPVVSKMVVWQGGKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7722

STRAIN 1169NT frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKLYLSHPKYMSLRSLWRTGNFVNKDFYYEVPKLDVDFDEAFKKSSIDFYAVATEMTS
 GKPEYFKIDSVEFQMEILRASSALPVVSKMVDWQGGKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIVRLEKNPDKLDSIYQLGMKDAKSVMPPELNSYLMK

SEQ ID NO. 7801

STRAIN 2603

ATGAAAGTTTGTAGTGTGATGATGAACCAGTTGCACGTAACGAATTAATTTACCTTCTT
 AATAAGTATGATTCTAACCTCGTTATAGCAGAGGCGCATGATATGGCTACTGCATTAGCT
 ATTTTACTTAGAGAAACTTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCT
 GGGTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACCATATTGATATTGCG
 ACTGCTTATGATCAATATGCTATTCAGGCTTTTGAGCATGATGCGCGTGATTATTTGTTA
 AAACCCATGATTTTGTAGAGCTAAAGCAAGCTATGGATAGAGTAAAAGGAGCGCTAAGT
 ACATCTACAATTATAGAGAGCGTAACCTCCGGTCCCTCTCTTCAAGCAACAGTATCCATTG
 ACAGTAGAAGATCGAATCTATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATG
 CAAGGAAAACCTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAA
 CAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTTACATTGTG
 AACATTAAATGCTATTAAAACGATTGAACCTTGGTTTAAACAAACACTTCAGTTACACCTT
 TGTAAATAAAATAACAGTTCCTGTAGCAGAGCAAATGTAAACCCCTAAAACAAATGTTA
 GGCATATCTACC

SEQ ID NO. 7802

STRAIN 090

AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTAA
 CGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAG
 AGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAAACTTTT
 GATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATT
 AGCAGAGTATATCAATAAAATGCCCAAACCACCATATTGATATTGCGA
 CTGCTTATGATCAATATGCTATTCAGGCTTTTGAGCATGATGCGCGTGAT
 TATTTGTTAAAACCCATGATTTTGTAGAGCTAAAGCAAGCTATGGATAG
 AGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCG
 GTCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTAT
 CTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAAC
 GATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAAC
 AATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCT
 TACATTGTGAACATTAATGCTATTAAAACGATTGAACCTTGGTTTAAACA
 AACACTTCAGTTACACCTTTGTAAATAAAATAACAGTTCCTGTTAGCAGAG
 CAAATGTAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7803

STRAIN A909

AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTAA
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAAACTTTTG
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCCAAACCACCATATTGATATTGCGGAC
 TGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGATGCGCGTGATT
 ATTTGTTAAAACCCATGAGTTTGTAGAGCTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCGG
 CCGTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACG
 ATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAACA

SEQUENCE LISTING

ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTGCACCGCTCTT
 ACATTGTGAATATTAATGCTATTAATAACGATTGAACCTTGGTTTAACCAA
 ACACCTTCAGTTACACCTTTTGTAAATAAAATAACAGTTCCTGTTAGCAGAGC
 AAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7804

STRAIN H36B

AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGT
 AACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGC
 AGAGGCGCATGATATGGCTACTGCATTAGCTATTTACTTAGAGAACTT
 TTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAA
 TTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTTATTGATATTCGC
 GACTGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGATGCGCGTG
 ATTATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAGCTATGGAT
 AGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACTTC
 CGGCCCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCT
 ATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAA
 CTGATTATACAAACACCTGATAAAAAATTATGAAATTGATGGCTCTCTACA
 ACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTGCACCGCT
 CTTACATTGTGAATATTAATGCTATTAACGATTGAACCTTGGTTTAAC
 CAAACACTTCAGTTACACCTTTGTAAATAAAATAACAGTTCCTGTTAGCAG
 AGCAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7805

STRAIN 18RS21

AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTAAC
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GGCGCATGATATGGCTACTGCATTAGCTATTTACTTAGAGAACTTTTG
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCCAAACCACCATTTATTGATATTTGCGAC
 TGCTTATGATCAATATGCTATTCAAGGCTTTTGAGCATGATGCGCGTGATT
 ATTTGTTAAACCCCTATGATTTTGATAGGCTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACTTCCGG
 TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACTG
 ATTATACAAACACCTGATAAAAAATTATGAAATTGATGGCTCTCTACAACA
 ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
 ACATTGTGAACATTAATGCTATTAACGATTGAACCTTGGTTTAACCAA
 ACACCTTCAGTTACACCTTTGTAAATAAAATAACAGTTCCTGTTAGCAGAGC
 AAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7806

STRAIN M732

AAAGTTTTAGTAGTTGATGATGAACCAGTT
 GCACGTAACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGT
 TATAGCAGAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAG
 AAATTTTGGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGG
 TTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTTATTGAT
 ATTCGCGACTGCTTATGATCAATATGCTATTCAAGGCTTTTGAGCAGGATG
 CGCGTGATTATTTGTTAAACCCCTATGAGTTTGATAGGTTAAAGCAAGCT
 ATGGATAGAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGT
 AGCTTCCGGTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATC
 GAATCTATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAA
 GGAAAACCTGATTATACAAACACCTGATAAAAAATTATGAAATTGATGGCTC
 TCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTAC
 ATCGCTCTTACATTGTGAATATTAATGCTATTAACGATTGAACCTTGG
 TTTAACCAAAACACTTCAGTTACACCTTTGTAAATAAAATAACAGTTCCTGT
 TAGCAGAGCAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7807

STRAIN COH1

AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTA
 ACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCA
 GAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAACTTT

SEQUENCE LISTING

TGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAAT
 TAGCAGAGTATATCAATAAAATGCCAAACCACCATTATTGATATTCGCG
 ACTGCTTATGATCAATATGCTATTCAGGCTTTTGAGCAGGATGCGCGTGA
 TTATTTGTTAAAACCCATGAGTTTGATAGGTTAAAGCAAGCTATGGATA
 GAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCC
 GGTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTA
 TCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAAC
 TGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAA
 CAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTC
 TTACATTGTGAATATTAATGCTATTAAAACGATTGAACCTTGGTTAACC
 AAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGA
 GCAAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7808

STRAIN M781

AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTAAC
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAACTTTTG
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCAAACCACCATTATTGATATTCGCGAC
 TGCTTATGATCAATATGCTATTCAGGCTTTTGAGCAGGATGCGCGTGATT
 ATTTGTTAAAACCCATGAGTTTGATAGGTTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCCGG
 TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACCTG
 ATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAACA
 ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
 ACATTGTGAATATTAATGCTATTAAAACGATTGAACCTTGGTTAACC
 ACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAGC
 AAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7809

STRAIN CJB110

CTTAATAAGTATGATTCTAACCTCGTTATAGCAGAGGCGCATGATATGGC
 TACTGCATTAGCTATTTTACTTAGAGAACTTTTGATGTAGCACTGTTAG
 ATATCCATCTCAGAGATGATTCTGGGTTGCAATTAGCAGAGTATATCAAT
 AAAATGCCAAACCACCATTATTGATATTCGCGACTGCTTATGATCAATA
 TGCTATTCAAGCTTTTGAGCATGATGCGCGTGATTATTTGTTAAAACCCCT
 ATGAGTTTGATAGGCTAAAGCAAGnTATGGATAGAGTAAAAGGAGCGCTA
 AGTACATCTACGAATTATAGAGAGCGTAACTTCCGGCCCTCTCTCAAGCA
 ACAGTATCCATTGACAGTAGAAGATnGAATCTATCTGGTGTGCGCGGATG
 ATATCCTTTTGATTGAAGCTATGCAAGGAAAACCTGATTATACAAACACCT
 GATAAAAATTATGAAATTGATGGCTCTCTACAACAATGGCAAGATAAACT
 ACCATCATCTCAATTTGTACGGGTGCACCGCTCTTACATTGTGAATATTA
 ATGCTATTAAAACGATTGAACCTTGGTTTAAACCAACACTTCAGTTACAC
 CTTTGTAAATAAAATAACAGTTCCTGTTAGCAGAGCAAATGTAAACCCCT
 AAAACAAATGTTAGG

SEQ ID NO. 7810

STRAIN 1169NT

AAAGTTTTAGTAGTTGATGATGAACCAG
 TTGCACGTAACGAATTAATTTATCTTCTTAATAAGTATGATTCTAACCTC
 GTTATAGCAGAGGCGCATGATATAGCTACTGCATTAGCTATTTTACTTAG
 AGAAACTTTTGATGTAGCACTGTAGATATCCATCTCAGAGATGATTCTG
 GGTGCAATTAGCAGAGTATATCAATAAAATGCCAAACCACCATTATTG
 ATATTGCGCACTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGA
 TGCGCGTGATTATTTGTTAAAACCCATGAGTTTGATAGGCTAAAGCAAG
 CTATGGATAGAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGC
 GTAACCTTCCGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGA
 TCGAATCTATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGC
 AAGGAAAACCTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGC
 TCTCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGT
 GCACCGCTCTTACATTGTGAATATTAATGCTATTAAAACGATTGAACCTT
 GGTTAACCACAACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCT

SEQUENCE LISTING

GTTAGCAGAGCAAATGTAAAACCCCTAAACAAATGTTAGGCATATCTAC
C

SEQ ID NO. 7811

STRAIN JM9130013

AAAGTTTTAGTAGTTGATGATGAACCACT

TGCACGTAACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCG
TTATAGCAGAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGA
GAAACTTTTGTAGTACTGTTAGATATCCATCTCAGAGATGATTCTGG
GTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTTATGA
TATTCGCGACTGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGAT
GCGCGTGATTATTTGTTAAAACCCCTATGAGTTTGATAGGCTAAAGCAAGC
TATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCG
TAACCTCCGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGAT
CGAATCTATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCA
AGGAAAACGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCT
CTCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTG
CACCGCTCTTACATTGTGAATATTAATGCTATTTAAACGATTGAACCTTG
GTTTAACCAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTG
TTAGCAGAGCAAATGTAAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7812

STRAIN 2603 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPELLIFATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST
STIIESVTSGLPKQYPLTVEDRIYLVSADDILLIEAMQGKLIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIAKTIEPWFNQTLQLHLCKNITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7813

STRAIN 090 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPELLIFATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST
STIIESVTSGLPKQYPLTVEDRIYLVSADDILLIEAMQGKLIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIAKTIEPWFNQTLQLHLCKNITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7814

STRAIN A909 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPELLIFATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPKQYPLTVEDRIYLVSADDILLIEAMQGKLIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIAKTIEPWFNQTLQLHLCKNITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7815

STRAIN H36B frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPELLIFATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPKQYPLTVEDRIYLVSADDILLIEAMQGKLIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIAKTIEPWFNQTLQLHLCKNITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7816

STRAIN 18RS21 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPELLIFATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST
STIIESVTSGLPKQYPLTVEDRIYLVSADDILLIEAMQGKLIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIAKTIEPWFNQTLQLHLCKNITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7817

STRAIN M732 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG

SEQUENCE LISTING

LQLAEYINKMPKPELLIFATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVASGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7818

STRAIN COH1 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPELLIFATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVASGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7819

STRAIN M781 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPELLIFATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVASGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7820

STRAIN CJB110 frame: 1

LNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG LQLAEYINKMPKPELLIF
ATAYDQYAIQAFEHDARDYLLKPYEFDRLKQXMDRVKGALSTSTIIESVTSGPLFKQQYP
LTVEDXIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQWQDKLPSSQFVRVHRSYI
VNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQML

SEQ ID NO. 7821

STRAIN 1169NT frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDIATLAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPELLIFATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7822

STRAIN JM9130013 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPELLIFATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7901

STRAIN 2603

ATGGGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCCGGCACTCCTTTTGAAGGG
CGTGCCCTTTTGGACGTCAATCTGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGG
CACACAGGTTCTGGAAAATCACTATTATGCAACTTTTGAATGGTTTACATATTCCTACA
AAAGGTGAGGTAATTGTGCGATGATTTTTCTATTAAAGCAGGGGACAAGAACAAGAAATC
AAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCAATTTCCAGAAAGTCAGCTTTTGA
GAGACAGTTTAAAGGATGTTGCTTTTGGACCACAAAATTTTGGTATTTCTCAGATTGAA
GCTGAAAGGCTGGCTGAAGAAAAATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGAT
AAAAATCCATTTGAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTA
GCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGA
AGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTATCGTCTTA
GTGACTCACTTAATGGACGATGTAGCGGATTAATGCTGACTATGTGTATGTTTTAGAAGCA
GGAAAGTAACCTTATCAGGACAACCAAAACAGATTTTCAAGAAGTAGAAGCTTTAGAA
AGTAAACAATTAGGAGTTCCCAAAATCACCAAGTTTGTCTCAAGACTATCTCATAAGGGA
TTAAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7902

STRAIN 090

GGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC

SEQUENCE LISTING

GGCACTCCTTTTGAAGGGCGTGCCCTTTTTTGACGTCAATCTGAAAATTGA
AGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAATCAA
CTATTATGCAACTTTTGAATGGTTTACATATTCTACAAAAGGTGAGGTA
ATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACAAGAAATCAA
ATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCAGAAAGTCAGC
TTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACCACAAAATTTT
GGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAGGTT
AGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTTGAACTTTCTG
GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGAACCC
AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGAAG
AAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAAGGAATGACTA
TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTAT
GTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAAACA
GATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTAGGAGTTCCCA
AAATCACCAGTTTGTCTAAAGACTATCTCATAAGGGATTAAATTTACCT
AGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7903

STRAIN A909

GGAATTGAATTTAAAAATGTAAGTTATACCTATCAA
GCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTTGACGTCAATCTGAAAAT
TGAAAGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAAT
CAACTATTATGCAACTTTTGAATGGTTTACATATTCTACAAAAGGTGAG
GTAATTGTGCGATGATTTTTCTATTAAAGCAGGGGACAAGAACAAGAAAT
CAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCAGAAAGTC
AGCTTTTTTGAAAGAGACAGTTTTTAAAGATGTTGCTTTTGGACCACAAAAT
TTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAG
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CTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGCGATGGAA
CCCAAAGTACTAGTACTAGATGAGCCAACAGCTGGACTTGATCCTAAGGG
AAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAAGGAATGA
CTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGAC
TATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAA
GCAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTAGGAGTTC
CCAAAATCACCAGTTTGTCTAAAGGCTATCTCATAAGGGATTAAATTTA
CCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAGCATGG
A

SEQ ID NO. 7904

STRAIN H36B

GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCACTCCTTTTTGAAGGGCGTGCCCTTTTTTGACGTCAATC
TGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCT
GGAATAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTACAAA
AGGTGAGGTAATTGTGATGATTTTTCTATTAAAGCAGGGGACAAGAACA
AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCA
GAAAGTCAGCTTTTTGAAGAGACAGTTTTTAAAGATGTTGCTTTTGGACC
ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTAGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
AACCAAAGCAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
GGAGTTCCCAAATCACCAGTTTGTCTAAAGGCTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7905

STRAIN 18RS21

GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCACTCCTTTTTGAAGGGCGTGCCCTTTTTTGACGTCAATC
TGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCT

SEQUENCE LISTING

GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTTACAAA
AGGTGAGGTAATTGTGCGATGATTTTTCTATTAAAGCAGGGGACAAGAACA
AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCA
GAAAGTCAGCTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACC
ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
AACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAACAATTA
GGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7906

STRAIN M732

GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC
TGAAAATTGAAGATGTTTCTTATACCGCGTTTCAATGGGCACACAGGTTCT
GGAAAATCAACTTTTATGCAACTTTTGAATGGTTTACATATTCTTACAAA
AGGTGAGGTAATTGTGCGATGATTTTTCTATTAAAGCAGGGGACAAGAACA
AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCA
GAAAGTCAGCTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACC
ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
AACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAACAATTA
GGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7907

STRAIN COH1

GGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
GGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATCTGAAAATTGA
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CTATTATGCAACTTTTGAATGGTTTACATATTCTTACAAAAGGTGAGGTA
ATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACAAGAAATCAA
ATTTATAAGGC AAAAGTTGGTTTAGTTTTTCAATTTCCAGAAAGTCAGC
TTTTTGAAGAGACAGTTTTTAAAGGATGTTGCTTTTGGACCACAAAATTTT
GGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAGGTT
AGTTGGTATCAGTGAGGATTTATTCGATAAAAAATCCATTTGAACTTTCTG
GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGAACCC
AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGAAG
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GTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAAACA
GATTTTTCAAGAAGTAGAACTTTTAGAAAGTAACAATTAAGGATTCCCA
AAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
AGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7908

STRAIN M781

GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC
TGAAAATTGAAGATGTTTCTTATACCGCGTTTCAATGGGCACACAGGTTCT
GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTTACAAA
AGGTGAGGTAATTGTGCGATGATTTTTCTATTAAAGCAGGGGACAAGAACA

SEQUENCE LISTING

AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCAATTTCCA
GAAAGTCAGCTTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACC
ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
AACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
GGAGTTCCCAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7909

STRAIN CJB110

GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCACTCCTTTTTGAAGGGCGTGCCCTTTTTGACGTCAATC
TGAAAATTGAAGATGCTTCCTATACCGCTTCATTGGGCACACAGGTTCT
GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAA
AGGTGAGGTAATTTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACA
AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCAATTTCCA
GAAAGTCAGCTTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACC
ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
AACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
GGAGTTCCCAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7910

STRAIN 1169NT

GGAATTGAATTTAAAAATGTAA
GTTATACCTATCAAGCCGGCACTCCTTTTTGAAGGGCGTGCCCTTTTTGAC
GTCAATCTGAAAATTGAAGATGCTTCCTATACCGCTTCATTGGGCACAC
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CTACAAAAGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGAC
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GAAGAAAAATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAA
TCCATTTGAACCTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTA
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CGGATTATGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTA
TCAGGACAACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAA
ACAATTAGGAGTTCCCAAATCACCAAGTTTGCTCAAAGACTATCTCATA
AGGGATTAAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAG
GCTATTAAGCATGGA

SEQ ID NO. 7911

STRAIN JM9130013

GGAATTGAATTTAAAAATGTAAGTT
ATACCTATCAAGCCGGCACTCCTTTTTGAAGGGCGTGCCCTTTTTGACGTT
AATCTGAAAATTGAAGATGCTTCCTATACCGCATTCATTGGGCACACAGG
TTCTGGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTA
CAAAAGGTGAGGTAATTTGTCGATGATTTTTCTATTAAAGCAGGGGACAAG
AACAAAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCAATT

SEQUENCE LISTING

TCCAGAAAGTCAGCTTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTG
 GACCACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAA
 GAAAAATTAAGGTTAGTTGGTATTAGTGAGGATTATTTCGATAAAAAATCC
 ATTTGAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTT
 TAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTT
 GATCCTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAAATCTTCATAA
 AAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGG
 ATTATGCTGACTATGTGTATGTTTTAGAACGAGGAAAGTAACCTTATCA
 GGACAACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAAGTAAACA
 ATTAGGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGG
 GATTAAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCT
 ATTAAGCATGGA

SEQ ID NO. 7912

STRAIN 2603 frame: 1

MGIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGVLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLVGI SEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEV ELLES
 KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7913

STRAIN 090 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGVLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLVGI SEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEV ELLES
 KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7914

STRAIN 090 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGVLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLVGI SEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEV ELLES
 KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7915

STRAIN H36B frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGVLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLVGI SEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEV ELLES
 KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7916

STRAIN 18RS21 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGVLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLVGI SEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEV ELLES
 KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7917

STRAIN M732 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGVLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLVGI SEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEV ELLES
 KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7918

STRAIN COH1 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK

SEQUENCE LISTING

GEVIVDDFSIKAGDKNKEIKFIRQKVGVLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEEKLRLVGI SEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEV ELLS
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7919

STRAIN M781 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTGSGKSTIMQLLNLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGVLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEEKLRLVGI SEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEV ELLS
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7920

STRAIN CJB110 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGVLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEEKLRLVGI SEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEV ELLS
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7921

STRAIN 1169NT frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGVLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEEKLRLVGI SEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEV ELLS
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7922

STRAIN JM9130013 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGVLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEEKLRLVGI SEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEV ELLS
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 8001

STRAIN 2603

GTGAACCACTTAACTCAGTAAAGAAAATATAGCTAAATAGATTTTGACTTTCTT
 AATGAGGCACTTAATGCAATATTCGTTTGAAAGAATTAGTAGATGAACATAAAATTTCA
 AAAGAAGTGGACAGTAAAGGTTGGTCCAAAAAGACTCTCGAACGATAAAATCTTGTAC
 GATGGCCTTATCAATAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCAA
 GTCATTCCATTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAAGGGAGAATTCT
 AAAAATTATAGAAATATACAACTACAGTGATTATGAAATGGAGTTAATCAATGAGGATAGG
 CAACAATTTTCAAAATATGAAACAGTTGATTTAGACCAATTGATACTTGTGATATTTT
 AATATTGATGACTACATTTTCATCATATTTAACAATA

SEQ ID NO. 8002

STRAIN H36B

AACCACTTACTTAACTCAGTAAAGAAAATATAGCT
 AAAATAGATTTTGACTTTCTTAATGAGGCACTTAATGCAATATTCGTTT
 GAAAGAATTAGTAGATGAACATAAAATTTCAAAGAAGTGGACAGTAAAG
 GTTGGTCCAAAAAGACTCTCGAACGATAAAATCTTGTACGATGGCCTT
 ATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCA
 AGTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAA
 GGGAGAATTCTAAAAATATAGAAATATACAACTACAGTGATTATGAAATG
 GAGTTAATCAATGAGGATAGGCAACAATTTTCAAAATATGAAACAGTTGA
 TTTAGACCAATTGATACTTGTGATATTTTAAATATTGATGACTACATTT
 CATCATATTTAACAATA

SEQ ID NO. 8003

STRAIN 18RS21

AACCACTTACTTAACTCAGTAAAGAAAATATAG

SEQUENCE LISTING

CTAAAATAGATTTTGACTTTCTTAATGAGGCACCTTAATGCAAATATTCGT
TTGAAAGAATTAGTAGATGAACATAAAATTTCAAAGAAGCTGGACAGTAA
AGGTTGGTCCAAAAAGACTCTCGAACGATAAAATCTTGACGATGGCC
TTATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATC
CAAGTCATTCCATTGCTAATGTACATGTACTACTGTTTTTAATACCAGA
AAGGGAGAATTCTAAAAATTATAGAATATACAACACAGTGATTATGAAA
TGGAGTTAATCAATGAGGATAGGCAACAATTTTCAAATATGAAACAGTT
GATTTAGACCAATTGATACTTGTGATATTTTAATATTGATGACTACAT
TTCATCATATTTAACAATA

SEQ ID NO. 8004

STRAIN 2603 frame: 1

VNHLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILY
DGLINKHIVSLDRADYNIIQVIPFANVHVLLFLIPERENSKNYRIYNSDYEMELINEDR
QQFSKYETVDLDQLILVDIFNIDDYISSYLT

SEQ ID NO. 8005

STRAIN H36B frame: 1

NHLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNIIQVIPFANVHVLLFLIPERENSKNYRIYNSDYEMELINEDRQ
QFSKYETVDLDQLILVDIFNIDDYISSYLT

SEQ ID NO. 8006

STRAIN 18RS21 frame: 1

NHLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNIIQVIPFANVHVLLFLIPERENSKNYRIYNSDYEMELINEDRQ
QFSKYETVDLDQLILVDIFNIDDYISSYLT

SEQ ID NO. 8101

STRAIN 090

AGCAAGCCTAATGTTGTTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTTCATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCCTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
TAACTAATAGAAGCTGAGAACCAGAAGTTGCTAGCAAAACAACATAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
CGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8102

STRAIN A909

AGCAAGCCTAATGTTGTTTCAGTTAAATAATCAATA
TATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCG
TTTAAATGGGTTGGGTTCTTATTTTGTTCATGCTtttATTTATTTTACCCACTTATAATTT
AGTTAAGAGTTACAGAACTTTACAAGAAGTCGTCGAAGAAGTTGTAAAATTAACGAAAGA
CTATCAGACATTAACTAATAGAAGCTGAGAACCAGAAGTTACTAGCAAAACAACATAAAAA
TCCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGACCGGCGAAAT
GATTTACCCATTACCAGACCT

SEQ ID NO. 8103

STRAIN H36B

AGCAAGCCTAATGTTGTTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTTCATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCCTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
TAACTAATAGAAGCTGAGAACCAGAAGTTACTAGCAAAACAACATAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
CGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8104

STRAIN 18RS21

AGCAAGCCTAATGTTGTTTCAGTTAAATAATCAATATATTAACGATGAGAATCTAAAAA
CGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTT

SEQUENCE LISTING

GTCATGCTTTTATTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACAA
 GAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACATTAACATAAGAACT
 GAGAACCAGAAGTTGCTAGCAAAACAACATAAAAAATCCAGATTACGTTCAAAAATATGCT
 CGAGCTAAGTATTATTTCTCTAAGACCGGCGAAATGATTTACCCATTACCAGACCTTTTA
 CCAAAA

SEQ ID NO. 8105

STRAIN M732

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTCATG
 CTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
 ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACATAAAAAAT
 CCAGATTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGAC
 CGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8106

STRAIN COH1

AGCAAGCCTAATGTTGTTTCAGTTAAATAATC
 AATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTA
 CGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTTGTCATGCTttt
 ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACAAG
 AACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACATTAAC
 AATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACATAAAAAATCCAGA
 TTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGACCGGCG
 AAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8107

STRAIN M781

AGCaAGCCTAATGTTGTTTCAGTT
 AAATAATCAATATaTTAACGATGAGAATCTAAAAAACGTTACGAAGCTG
 AGGAGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTTGTC
 ATGCTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAAC
 TTTACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGA
 CATTAATAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACATAAAA
 AATCCAGATTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAA
 GACCGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8108

STRAIN CJB110

AGCAAGCCTAATGTTGTTTCAGTTAAATAATC
 AATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTA
 CGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTTGTCATGCTttt
 ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACAAG
 AACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACATTAAC
 AATAGAACTGAGAACCAGAAGTTGCTAGCAAAACAACATAAAAAATCCAGA
 TTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGACCGGCG
 AAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8109

STRAIN 1169NT

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTTGTCATG
 CTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
 ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACATAAAAAAT
 CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 CGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8110

STRAIN JM9130013

AGCaAGCCTAATGTTGTTTCAGTTAAA

SEQUENCE LISTING

TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTTCATG
 CTTTATTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAAGCTT
 ACAAGAACGTCGTCAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAACAATAAAAAAT
 CCAGATTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGAC
 TGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8111

STRAIN 2603

agcaagcctaattgttgcagttaataatcaatatattaacgatgagaa
 tctaaaaaacggttacgaagctgaggagttacgccgaaaaaatcgtttaa
 tgggttgggttcttatttttgcctgcttttatttattttaccacttat
 aatttagttaagagttacagaactttacaagaacgtcgtaagaagttgt
 aaaattaacgaaagactatcagacattaactaatagaactgagaaccaga
 agttgctagcaaaacaactaaaaaatccagattacgttcaaaaatatgct
 cgagctaagtattatttctcctaagaccggcgaaatgattaccattacc
 agaccttttaccacaaa

SEQ ID NO. 8112

STRAIN 090

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
 VKSYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8113

STRAIN A909

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
 VKSYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
 IYPLPD

SEQ ID NO. 8114

STRAIN H36B

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
 VKSYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8115

STRAIN 18RS21

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNLVKSYRTLQ
 ERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM IYPLPDLL
 PK

SEQ ID NO. 8116

STRAIN M732

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
 VKSYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8117

STRAIN COH1

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNLVK
 SYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM IY
 PLPDLLPK

SEQ ID NO. 8118

STRAIN M781

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
 LVKSYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGE
 MIYPLPDLLPK

SEQ ID NO. 8119

STRAIN CJB110

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNLVK

SEQUENCE LISTING

SYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEMII
PLPDLLPK

SEQ ID NO. 8120

STRAIN 1169NT

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
VKSRYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
IYPLPDLLPK

SEQ ID NO. 8121

STRAIN JM9130013

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
VKSRYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
IYPLPDLLPK

SEQ ID NO. 8122

STRAIN 2603

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVKSRYRTLQ
ERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEMIIYPLD
LLPK

SEQ ID NO. 8201

STRAIN 2603

ATGAAAAATTTATTGTTAAAATGTAAGGATAAGAAGGTTAAAGCATTTACACTTTTAGAA
TGTTTGGTAGCATTGGTTACAATCACAGGAGCTTTACTAGTTTATCAAGGACTGACAAA
TTGTTGGCTCAACAGATAGTAGTGATGTCTTCTCCAGTCAGTCTGAATGGGTGTATTA
ACTCAGCAACTAAATGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAA
CTTTATTTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTTC
CGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAGACAATTGT
CAAATGAGTCAGACCAAAAGTATGGTAAAACCTGTTTTTTATTTTAAGGACGGGTAAAA
AGGACATTTTACTATGATTTTAAAGAAGAACTTAA

SEQ ID NO. 8202

STRAIN 090

AATT CGAAGGCGCTCACTTGGAATATTTAAGACAGAACAACTTTATTTA
CGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTT
CCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGT
TAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACCTGTTTTT
TATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGA
AACT

SEQ ID NO. 8203

STRAIN A909

CAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTTAT
TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
TTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATG
GGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACCTGTT
TTTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGA
AGAAACT

SEQ ID NO. 8204

STRAIN H36B

ATGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTT
TATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGA
TGATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTT
ATGGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACCT
GTTTTTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAA
AGAAGAACT

SEQ ID NO. 8205

STRAIN 18RS21

AGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTTAT
TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
TTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATG

SEQUENCE LISTING

GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACCTTGTTT
TTTATTTTAAAGGACGGGTAAAAAGGACATTTTACTATGATTTTAAAGAA
GAAACT

SEQ ID NO. 8206

STRAIN M732

CAGAATTCGAAGGCGCTCACTTGGGAATATTTAAGACAGAACAAACTTTAT
TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
TTTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATG
GGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACCTTGTT
TTTATTTTAAAGGACGGGTAAAAAGGACATTTTACTATGATTTTAAAGA
AGAAACT

SEQ ID NO. 8207

STRAIN COH1

GAATTCGAAGGCGCTCACTTGGGAATATTTAAGACAGAACAAACTTTATTT
ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
TCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATGGG
TTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACCTTGTTTT
TTATTTTAAAGGACGGGTAAAAAGGACATTTTACTATGATTTTAAAGAAG
AAACT

SEQ ID NO. 8208

STRAIN M781

AGAATTCGAAGGCGCTCACTTGGGAATATTTAAGACAGAACAAACTTTATTT
TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
TTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATGG
GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACCTTGTTT
TTTATTTTAAAGGACGGGTAAAAAGGACATTTTACTATGATTTTAAAGAA
GAAACT

SEQ ID NO. 8209

STRAIN CJB110

GAATTCGAAGGCGCTCACTTGGGAATATTTAAGACAGAACAAACTTTATTT
ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
TCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGG
TTAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACCTTGTTTT
TTATTTTAAAGGACGGGTAAAAAGGACATTTTACTATGATTTTAAAGAAG
AAACT

SEQ ID NO. 8210

STRAIN 1169NT

TCGAAGGCGCTCACTTGGGAATATTTAAGACAGAACAAACTTTATTTACGT
AAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTTTCG
TAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAG
ACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACCTTGTTTTTAT
TTTAAAGGACGGGTAAAAAGGACATTTTACTATGATTTTAAAGAAGAAAC
T

SEQ ID NO. 8211

STRAIN JM9130013

TGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAACTTT
ATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGAT
GATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTA
TGGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACCTTG
TTTTTTATTTTAAAGGACGGGTAAAAAGGACATTTTACTATGATTTTAA
GAAGAACT

SEQ ID NO. 8212

STRAIN 2603 frame: 1

MKNLLKCKDKKVKAFLLLECLVALVTITGALLVYQGLTKLLAQQIVVMSSSSQSEWVLL
TQQLNAEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNC
QMSQTKSMVKLVFYFKDGLKRTFYDFKEET.

SEQUENCE LISTING

SEQ ID NO. 8213

STRAIN 090 frame: 3

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKS
SMVKLVFVYFKDGLKRTFYDFKEET

SEQ ID NO. 8214

STRAIN A909 frame: 3

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFVYFKDGLKRTFYDFKEET

SEQ ID NO. 8215

STRAIN H36B frame: 3

AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFVYFKDGLKRTFYDFKEET

SEQ ID NO. 8216

STRAIN 18RS21 frame: 2

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFVYFKDGLKRTFYDFKEET

SEQ ID NO. 8217

STRAIN M732 frame: 3

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFVYFKDGLKRTFYDFKEET

SEQ ID NO. 8218

STRAIN COH1 frame: 1

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFVYFKDGLKRTFYDFKEET

SEQ ID NO. 8219

STRAIN M781 frame: 2

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFVYFKDGLKRTFYDFKEET

SEQ ID NO. 8220

STRAIN CJB110 frame: 1

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFVYFKDGLKRTFYDFKEET

SEQ ID NO. 8221

STRAIN 1169NT frame: 3

EGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKSM
VKLVFVYFKDGLKRTFYDFKEET

SEQ ID NO. 8222

STRAIN JM9130013 frame: 2

AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFVYFKDGLKRTFYDFKEET

SEQ ID NO. 8301

STRAIN 2603

atgaaaaagattcgattatcaaagttttattaaaaatgattgttggtattttgtttttaatt
agtgtagcagctagttttttttttttccacgttgcccaagttcgagatgataaatccttt
atttcaaatggtcaacgtaagcctggaaactctttatatgcttatgataaatcctttgat
aagctattaaagcaaaaaatagaaatgacaaaccaaataaaagcaagttgcttggtat
gttcctgctgttaagaaaactcataagacagctgttgctcgttcattggttttcgaatagc
aaagagaatatgaaggcatatggttggtgtttcataagttaggataacaatgttccttatg
cctgacaatatgtcacatggtgaaagtcattgggcagttgataggctatggctggacgac
cgcgagaacattatcaaatggacagaaatgatagttgataagaatccatcaagccaaatt
actttatttgggtgtttcaatgggtggagcaacagtcattgatggctagtggtgaaaaatta
cctagtcaggttggttaatatcattgaagattgcggttattctagtggttggtggaatta
aaatttcaggctaaagagatgtatggtttaccagccttcccactcttatatgaagtttca
acaatttctaaaatcagagcaggttttttcgtatggacaagcaagtagtgctgaacaattg

SEQUENCE LISTING

aaaaagaataatttaccagccctctttatcatggtgataaggataattttgttccaaca
 agtatggtttatgacaactataaagctacagcaggttaagaaagagctttatattgtaaaa
 ggggcaaaacatgcgaaatcttttgaaacagagccagaaaaatatgagaaacgtatctct
 agttttttgaaaaaatatgaaaaa

SEQ ID NO. 8302

STRAIN 090

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCG
 AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
 TATATGCTTATGATAAATCCTTTGATAAGCTATTAAGCAAAAAATAGAA
 ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAA
 GAAAACTCATAAGACAGCTGTTGTCTGTTTCATGGTTTTGCGAATAGCAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 cTTATGCCTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCaAATGGACAGAAATGATAG
 TTGATAAGAATCCATCAAGCCAAATTACTTTaTTTTGGTGTTCATGGGT
 GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
 TAATATCATTGAAGATTGCGGTTATTCTAGTGTGTTGGGATGAATTAAAA
 TTTAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAA
 GTTTCAACAATTTCTAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
 TAGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCTCTTTATTCATG
 GTGATAAGGATAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAA
 GCTACAGCAGGTAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGC
 GAAATCTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
 TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8303

STRAIN A909

AATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTTATATGCT
 TATGATAAATCCTTTGATAAGCTATTAAGCAAAAAATAGAAATGACAAA
 CCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAACTC
 ATAAGACAGCTGTTGTCTGTTTCATGGTTTTGCGAATAGCAAAGAGAATATG
 AAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTATGCC
 TGACAACATTGCAACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCT
 GGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGTTGATAAG
 AATTCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTGGAGCAAC
 AGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTAATATCA
 TTGAAGATGCGGTTATTCTGGTGTGTTGGGATGAATTAAAAATTCAGGCT
 AAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAGTTTCAAC
 AATTTCTAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGTAGTGTGCG
 AACAATTGAAAAAGAATAATTTACCAGCCTCTTTATTCATGGTGATAAG
 GATAATTTTGTTCACAAGATATGGTTTATGACAACTATAAAGCTACAGC
 AGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCGAAATCTT
 TTGAAGACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTGAAG
 AAATATGAAAAA

SEQ ID NO. 8304

STRAIN H36B

AGTTTTTATTTTTTCCACGTTGCCCAAGTTCGAGATGATAAATCCTTTAT
 TTCAAATGGTCAACGTAAGCCTGGAAACTCTTTATATGCTTATGATAAAT
 CCTTTGATAAGCTATTAAGCAAAAAATAGAAATGACAAACCAAAATATA
 AAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAACTCATAAGACAGC
 TGTTGTCTGTTTCATGGTTTTGCGAATAGCAAAGAGAATATGAAGGCATATG
 GTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTATGCCTGACAACATT
 GCACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCTGGAACGACCG
 CGAGAACATTATCAAATGGACAGAAATGATAGTTGATAAGAATTCATCAA
 GCCAAATTACTTTATTTGGTGTTCATGGGTGGAGCAACAGTCATGATG
 GCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTAATATCATTGAAGATTG
 CGGTTATTCTGGTGTGTTGGGATGAATTAAAAATTCAGGCTAAAGAGATGT
 ATGGTTTTACCAGCCTTCCCACTCTTATATGAAGTTTCAACAATTTCTAAA
 ATCAGAGCAGGTTTTTCGTATGGACAAGCAAGTAGTGTGCAACAATTGAA
 AAAGAATAAATTTACCAGCCTCTTTATTCATGGTGATAAGGATAATTTTG
 TTCCAACAAGTATGGTTTATGACAACTATAAAGCTACAGCAGGTAAGAAA
 GAGCTTTATATTGTAAAAGGGGCAAAACATGCGAAATCTTTGAAACAGA

SEQUENCE LISTING

GCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAAAAaTATgAAA
AA

SEQ ID NO. 8305

STRAIN 18RS21

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGA
GATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
ATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGTTAAG
AAAACCTATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAGA
GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTTC
TTATGCTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
AATATCATTGAAGATTGCGGTTATTCTAGTGTGGGATgAATTAAAAATT
TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
AGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGG
TGATAAGGATAATTTTGTTCACAAGTATGGTTTATGACAACATAAAG
CTACAGCAGGTAAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
AAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
TTTGAAAAAATATGAAAAA

SEQ ID NO. 8306

STRAIN M732

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGA
GATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
ATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAG
AAAACCTATAAGACAGTTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAGA
GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTTC
TTATGCTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
GGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGTG
GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
AATATCATTGAAGATTGTGGTTATTCTAGTGTGGGATGAATTAAAAATT
TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
AGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTcTTTATTCATGG
TGATAAGGATAATTTTGTTCACAAGTATGGTTTATGACAACATAAAG
CTACAGCAGGTAAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
AAATCTTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
TTTGAAAAAATATGAAAAA

SEQ ID NO. 8307

STRAIN COH1

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTC
GAGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCT
TTATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGA
AATGaCAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTA
AGAAAACCTATAAGACAGTTGTTGTCGTTTCATGGTTTTGCGAATAGCAAA
GAGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGT
TCTTATGCTGACAAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAG
GCTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATA
GTGGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGG
TGGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTG
TTAATATCATTGAAGATTGTGGTTATTCTAGTGTGGGATgAATTAAAA
TTTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGA
AGTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAA
GTAGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTcTTTATTCAT
GGTGATAAGGATAATTTTGTTCACAAGTATGGTTTATGACAACATAA
AGCTACAGCAGGTAAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATG
CGAAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGT

SEQUENCE LISTING

TTTTTGAAAAAATATGAAAAA

SEQ ID NO. 8308

STRAIN M781

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCG
AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
TATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
ATGACAAACCAAAATATAAGCAAGTTGCTTGGTATGTTCTGCTGCTAA
GAAAACTCATAAGACAGTTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAG
AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
CTTATGCCTGACAACATTCACATGGTGAAAGTCATGGGCAGTTGATAGG
CTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAG
TGGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGT
GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
TAATATCATTGAAGATTGTGGTTATTcTAGTGTTTGGGATgAATTAAAAAT
TTCAGGcTAAAGAGATGTATGGTTTACCAGCCTTCCCACTcTTATATGaA
GTTTCAAcAATTTcTAAAAATcAgAGCAGGTTTTTCGTATGGACaAgCAAG
TAgtGTGCAACAATtGAAAAAGAATAATTTACCAGCCCTcTTTATTCATG
GTGATAAGGATAATTTTGTTCACAAcAGTATGGTTTATGaCAaCTATAAA
GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGGCAAAACATGC
GAAATCTTTTGAAAcCAGAGCCAGAAaAATATGAGAAACGTATCTCTAGTT
TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8309

STRAIN CJB110

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGAG
ATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTTA
TATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAAT
GACAAACCAAAATATAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGA
AAACTCATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAGAG
AATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTcT
TATGCCTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGCT
ATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGTT
GATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTGG
AGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTA
ATATCATTGAAGATTGCGGTTATTcTAGTGTTTGGGATgAATTAAAAATTT
CAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAGT
TTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACaAgCAAGTA
gTGTCGAACAATtGAAAAAGAATAATTTACCAGCCCTcTTTATTCATGGT
GATAAGGATAATTTTGTTCACAAAGTATGGTTTATGACAACCTATAAAGC
TACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGGCAAAACATGCGA
AATCTTTTGAAAcCAGAGCCAGAAaAATATGAGAAACGTATCTCTAGTTTT
TTGAAAAAATATGAAAAA

SEQ ID NO. 8310

STRAIN 1169NT

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGA
GATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
ATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
TGACAAACCaAAATATAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAG
AAAACTCATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAAtAGCAAAGA
gAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTc
TTATACCTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
AATATCATTGAAGATTgCGGTTATTcTAGTGTTTGGGATgAATTAAAAAT
TCAGGCTAaAGAGATGTATGGTTTaCCAGCCTTCCCACTcTTATATGAAG
TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACaAGCAAGT
AGTGTAGAACAATtGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGG
TGATAAGGATAATTTTGTTCACAAAGTATGGTTTATGACAACCTATAAAG
CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGGCAAAACATGCG
AAATCTTTTGAAAcCAGAGCCAGAAaAATATGAGAAACGTATCTCTAGTTT
TTTGAAAAAATATGAAAAA

SEQUENCE LISTING

SEQ ID NO. 8311

STRAIN JM9130013

GCTAGTTTTTTATTTTTTCCACGTTGCCCAAGTTTCG
 AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
 TATATGCTTATGATAAATCCTTTGATAAGCTATTAAGCAAAAAATAGAA
 ATGaCAAACCAAAATATAAGCAAGTTGCTTGGTATGTTCTGCTGTAA
 GAAAACCTATAAGACAGCTGTTGTCGTTTCATGGTTTTCGGAATAGCAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 CTTATGCCTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCaAATGGACAGAAATGATAG
 TTGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGT
 GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTGT
 TAATATCATTGAAGATTGCGGTTATTcTAGTGTTCGGATgAATTAAAT
 TTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAA
 GTTTCACAAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
 TAGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCTCTTTATTCATG
 GTGATAAGGATAATTTTGTTCACAAGTATGGTTTATGACAACATATAAA
 GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGC
 GAAATCTTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
 TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8312

STRAIN 2603 frame: 1

MKKIRLSKFIKMIVVILFLISVAASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFD
 KLLKQKIEMTNQNIKQVAWYVPAVKKTHKTAVVVHGFANSKENMKAYGWL FHKLGYNVLM
 PDNIAHGESHGQLIGYWNDRNI IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKL
 PSQVVNIIEDCGYSSVWDELKFKQAKEMYGLPAFPPLLYEVSTISKIRAGFSYQASSVEQL
 KKNL PALFIHGDKDNFVPTSMVYDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKEYE

SEQ ID NO. 8313

STRAIN 090 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTHKTAVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYWNDRNI
 IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFKQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQASSVEQLKKNL PALFIHGDKDNFVPTSMVY
 DNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKEYE

SEQ ID NO. 8314

STRAIN A909 frame: 3

SFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPAKKTHKTAVVVHGFAN
 SKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYWNDRNI IKWTEMIVDKN SSS
 QITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSGVWDELKFKQAKEMYGLPAFPPLLYE
 VSTISKIRAGFSYQASSVEQLKKNL PALFIHGDKDNFVPTSMVYDNYKATAGKKELYI
 VKGAKHAKSFETEPEKEYEKRISSFLKKEYE

SEQ ID NO. 8315

STRAIN H36B frame: 1

SFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 KKTHKTAVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYWNDRNI
 IKWTEMIVDKN SSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSGVWDELKFKQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQASSVEQLKKNL PALFIHGDKDNFVPTSMVY
 DNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKEYE

SEQ ID NO. 8316

STRAIN 18RS21 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 VKKTHKTAVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYWNDRNI
 IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFKQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQASSVEQLKKNL PALFIHGDKDNFVPTSMVY
 DNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKEYE

SEQ ID NO. 8317

SEQUENCE LISTING

STRAIN M732 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTHKTVVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDREN
 IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLP SQVVNI IEDCGYSSVWDELKFQ
 AKEMYGLPAFP LLYEVSTISKIRAGFSYQG ASSVEQLKKNL PALFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRIS SFLKKEYE

SEQ ID NO. 8318

STRAIN COH1 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTHKTVVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDREN
 IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLP SQVVNI IEDCGYSSVWDELKFQ
 AKEMYGLPAFP LLYEVSTISKIRAGFSYQG ASSVEQLKKNL PALFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRIS SFLKKEYE

SEQ ID NO. 8319

STRAIN M781 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTHKTVVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDREN
 IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLP SQVVNI IEDCGYSSVWDELKFQ
 AKEMYGLPAFP LLYEVSTISKIRAGFSYQG ASSVEQLKKNL PALFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRIS SFLKKEYE

SEQ ID NO. 8320

STRAIN CJB110 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTHKTA VVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDREN
 IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLP SQVVNI IEDCGYSSVWDELKFQ
 AKEMYGLPAFP LLYEVSTISKIRAGFSYQG ASSVEQLKKNL PALFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRIS SFLKKEYE

SEQ ID NO. 8321

STRAIN 1169NT frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTHKTA VVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDREN
 IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLP SQVVNI IEDCGYSSVWDELKFQ
 AKEMYGLPAFP LLYEVSTISKIRAGFSYQG ASSVEQLKKNL PALFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRIS SFLKKEYE

SEQ ID NO. 8322

STRAIN JM9130013 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 VKKTHKTA VVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDREN
 IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLP SQVVNI IEDCGYSSVWDELKFQ
 AKEMYGLPAFP LLYEVSTISKIRAGFSYQG ASSVEQLKKNL PALFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRIS SFLKKEYE

SEQ ID NO. 8401

STRAIN 2603

ATGATGAAAGTTT TAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACTAAAC
 AATATGGAATGTT TAGCGACTGTCACTATCAATATCAAAAAGAATCATAGCATTAATTTG
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 ATCGTAGTAGCAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCA
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 GTTTATGTTGGTTTCTATCAAAATGGTGATACTGTAAACCAGACTGT CACACTTCTCTT
 GAAGAAGTCTTACAAGAGGTGGGGAATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCA
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 TGTGCAGTAGCAATTGGGCGCAAGGACAAAAAATGAAAAGCGTTAATGTAGATGCGTTT
 GTTCCACGATACTTAAACGTGTTGAAGCTGAGGAAAATTGGTTAAAAAACCCTGTGAA
 ACGAATACAGAAAGATATATTAAGAGAGTT

SEQ ID NO. 8402

STRAIN 090

SEQUENCE LISTING

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACT
 AAACAATATGGAATGTTTAGCGACTGTCACTaTCAATATCAAAAAGAATC
 ATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGCAATCAATTGAT
 TTAGAACCTCAAGATTTGGACCGTATCGTAGTGGCAGAGGGTCCAGGATC
 TTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAATGCTAGCTTATA
 CGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTTAACAAT
 GGATTTTTCAGAAAATGATTTGTTGGTACCACTTATAGATGCACGACGTAA
 CAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGTTAAACCgACT
 GTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGAATAAAGCCAAT
 GTTCATTTTGTCTGGAGAGGTTGCAGCATTTTTTGATCAGATTAAgAAAGC
 CTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCAGTGGCAATTG
 GCGCAAAGGACAAAAAATGGAAGCGTTAATGTAGATGCGTTTGTCCA
 CGATACTTAAAACGAGTTGAAGCTGAGGAAAATTTGGTTAAAAAACCACTG
 TGAACGAAT

SEQ ID NO. 8403

STRAIN A909

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCAG
 TGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATATC
 AAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGCA
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 GTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAATG
 CTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGC
 TTTAACAAATGGATTTTCAGAAAATGATTTATTTGGTACCACTTATAGATG
 CACGACGTAAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGTT
 AAACCAGACTGTACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGAA
 TAAAGCCAATGTTCAATTTTGTCTGGAGAGGTTGCAGCATTTGTTGACCAGA
 tTAAgAAAGTTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCA
 GtGGCAATTGGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAGATGC
 GTTTGTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTTGGTTAA
 GAAACCACTGTGAAACGAAT

SEQ ID NO. 8404

STRAIN H36B

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
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 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAACAAATGGATTTTCAGAAAATGATTTATTTGGTACCACTTATAGAT
 GCACGACGTAAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
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 ATAAAGCCAATGTTTCATTTTGTCTGGAGAGGTTGCAGCATTTGTTGACCAG
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 AGTGGCAATTGGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTTGGTTA
 AGAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8405

STRAIN 18RS21

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 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
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 CTTTAACAAATGGATTTTCAGAAAATGATTTATTTGGTACCACTTATAGAT
 GCACGACGTAAATAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGT
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 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
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SEQUENCE LISTING

AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8406

STRAIN M732

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACATCAATAT
CAAAAAGAATCATAGCATTAATTTGATGCCAGCCATTGATTTTTTAATGC
AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAAT
GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTATAGAT
GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGT
TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTTCAATTTTGTGCGAGAGGTTGCAGCATTTTTTGTATCAG
ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
AGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGAnn
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AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8407

STRAIN COH1

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCAC
TATCAGTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACATC
AATATCAAAAAGAATCATAGCATTAATTTGATGCCAGCCATTGATTTTTT
AATGCAATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAG
CAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCA
AAAATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCT
GTACGCTTTAAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTA
TAGATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGAT
ACTGTTAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGT
GGGGAATAAAGCCAATGTTTCAATTTTGTGCGAGAGGTTGCAGCATTTTTTG
ATCAGATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCT
TGTGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGT
AGATGCGTTTTGTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATT
GGTTAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8408

STRAIN M781

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTA
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TGCAATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTATCA
GAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAA
AATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGT
ACGCTTTAAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTATA
GATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATAC
TGTTAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGG
GGAATAAAGCCAATGTTTCAATTTTGTGCGAGAGGTTGCAGCATTTTTGTAT
CAGATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTG
TGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAG
ATGCGTTTTGTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGG
TTAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8409

STRAIN CJB110

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGtaCTAAACAATATGGAATGTTTAGCGACTGTCACATCAATAT
CAAAAAGAATCATAGCATTAATTTGATGCCAGCCATTGATTTTTTAATGC
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GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAAACAAATGGATTTTCAGAAAATGATTTGTTGGTACCACTTATAGAT
GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGT
TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA

SEQUENCE LISTING

ATAAAGCCAATGTTTCATTTTGTCTGGAGAGGTTGCAGCATTTTTtgATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTGGCAATTGGGCGCAAAGGACAAAAAATGGAAAGCGTTAATGTAgATG
 CGTTTGTTCACGATACTTAAACGAGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8410

STRAIN 1169NT

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACATCAATAT
 CAAAAAGAATCATAGCATTAATTTGATGCCAGCCaTTGATTTTTTAATGC
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 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAACAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGAT
 GCACGACGTAAACAATGTTTATGTTGGTTTCTATCAAAATGGTGACTGT
 TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTCTGGAGgAGGTTGCAGCATTGTGACCAG
 ATTAAGAAAGCTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTGGCAATTGGGCGCAAAGGACAAAAAATGGAAAGCGTTAATGTAgATG
 CGTTTGTTCACGATACTTAAACGTTGTAAGCTGAAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8411

STRAIN JM9130013

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACATCAATAT
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 gCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAACAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGAT
 GCACGACGTAAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
 TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTCTGGAGAGGTTGCAGCATTGTGACCAG
 ATTAAGAAAGTTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTGGCAATTGGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACTTAAACGTTGTAAGCTGAGGAAAATTGGTTA
 AGAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8412

STRAIN 2603 frame: 1

MMKVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDR
 IVVAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNN
 VYVGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLP
 CAVAIGRKGQMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8413

STRAIN 090 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLP
 CAVAIGRKGQMKSVNVDAFVPRYLKRVEAEENWLKNHCETN

SEQ ID NO. 8414

STRAIN A909 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLP
 CAVAIGRKGQMKSVNVDAFVPRYLKRVEAEENWLKNHCETN

SEQ ID NO. 8415

STRAIN H36B frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV

SEQUENCE LISTING

VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFVDQIKKVLPHAKITETLPCA
 VAIGRKGQKMKSVNVDADFVPRYLKRVEAEENWLRNHCETNTEEYIKRV

SEQ ID NO. 8416

STRAIN 18RS21 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDADFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8417

STRAIN M732 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNXXFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8418

STRAIN COH1 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDADFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8419

STRAIN M781 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VSEGPSTYGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDADFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8420

STRAIN CJB110 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMSVNVDADFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8421

STRAIN 1169NT frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMSVNVDADFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8422

STRAIN JM9130013 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKVLPHAKITETLPCA
 VAIGRKGQKMKSVNVDADFVPRYLKRVEAEENWLRNHCETNTEEYIKRV

SEQ ID NO. 8501

STRAIN 2603

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 ggtaatcgagcaactgtcacagttaaagtgggtgataaaatcacagctggtcagcagtta
 gttcaatatgataacaactgcacaagcagcctacgacactgctaatacgctcaattaaat
 aaagtagcgcgtcagattaataatctaaagacaacaggaagtcctccagctatggaatca
 agtgcataactctcttcacatcacaaaggacaagggaactcaatcgactagtggtgcgacg
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SEQUENCE LISTING

gatttgaatgatgcttatgcagatgcacaggcagaagtaataaagcacaaaaagcattg
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SEQ ID NO. 8502

STRAIN 090

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CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAAGGTAATCGAGCAACTGTCACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTTCAGCAGTTAGTTCATATGATACAACAACCTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAATAATCTA
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ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCAGCAATCGTC
TACAGCAAAATTATCAAGTCAAGCTAATGCTTCATACAACCAACAACCTT
CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
ACAAAAGCATTTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTAGTCAAGTA
CTTGTCCTATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
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TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
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TTGGGTATACAAATGATTCTAATCGTAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAAATCGTGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG

SEQ ID NO. 8503

STRAIN A909

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAA
CTACAAAGTTTTTAAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTT
TGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCT
AATAAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCAC
AGCTGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCT
ACGACACTGCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAATAAT
CTAAAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTC
ATCATCATCACAAGGACAAGGGGCTCAATCGACTAGTGGTGCAGCAATC
GTCTACAGCAAAATTATCAAGTCAAGCTAATGCTTCATACAACCAACAA
CTTCAAGATTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAA
AGCACAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGA
CAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTAGTCAA
GTACTTGTCCTATGAGCAACTGAGGGTAACTCCAAGTACAAGGAACGAT
GAGTGAGTATGATTTGGCTAATGTTAAAAAAGACCAGTCTGTTAAATAA
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TCAAATTATCCAGAAGCAGAAGCAACCAACAATGACTCTAATAACGGCTC
TAGTGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATG
CATTAACAACAGGTTTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAG
CACCTTATTGTTCTTACAAGTTCTGTGACAAAACAAGATAATAAACAACCT
TGTTTGGGTATACAATGATTCTAATCGTAAAATTTCCAAAGTTGAAGTCA
AAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAA
GCAGGACAATCGTGTTACTAATCCAAGCAAACTTTCAAGGATGGGCA
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SEQUENCE LISTING

AGGTGAAA

SEQ ID NO. 8504

STRAIN H36B

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
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CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAGGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCTT
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GGACAAATCGTAGTTACTAATCCAAGTAAAGCTTTCAAGGATGGGCAAAA
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TG

SEQ ID NO. 8505

STRAIN 18RS21

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
CAAAGTTTTTAAATGTTAGAGAAGGAAGTGTTTCGTCCTCAACTCTTTTGA
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TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCTTC
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TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
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AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAG

SEQ ID NO. 8506

STRAIN M732

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
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CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
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TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGGAGTTTTTCCAGCTATGGAATCAAGTGATCAATCTTCATC

SEQUENCE LISTING

ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACTT
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TGAA

SEQ ID NO. 8507

STRAIN COH1

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CAGAGGTGAA

SEQ ID NO. 8507

STRAIN M781

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CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
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SEQUENCE LISTING

TAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
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TGAA

SEQ ID NO. 8508

STRAIN CJB110

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AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
TGA

SEQ ID NO. 8509

STRAIN 1169NT

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CAAAAAATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATC
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SEQ ID NO. 8510

STRAIN JM9130013

SEQUENCE LISTING

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 ACGTGTCAATCGTCAATTAATAAAGTAGCGCGTCAGATTAATAATCTA
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 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAGCA
 GGACAAATCGTGGTTACTAATCCAAAGCAAACTTTCAAGGATGGGCAAAA
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 TGAAA

SEQ ID NO. 8511

STRAIN 2603 frame: 1

MSKRQNLGISKKGAIISGLSVALIVVIGGFLWVQSQPNKSAVKNTNYKVFNVREGSVSSST
 LLTGKAKANQEYVYFDANKGNRATVTVKVGDKITAGQQLVQYDTTTAQAAAYDTANRQLN
 KVARQINNLTGSLPAMESSDQSSSSSQGGTQSTSGATNRLQQNYQSQANASYNQQLQ
 DLNDAYADAQAEVNKAQKALNDTVITSDVSGTVVEVNSDIDPASKTSQVLVHVATEGKLG
 VQGTMSSEYDLANVKKDQAVKIKSKVYPDKKEWEGKISYISNYPEAEANNNDNSNGSSAVNY
 KYKVDITSPLDALKQGFTVSVEVNGDKHLIVPTSSVINKDNKHFVWVYNDNSNRKISKVE
 VKIGKADAKTQEILSGLKAGQIVVTNPSKTFKDGQKIDNIESIDLNSNKKSEV

SEQ ID NO. 8512

STRAIN 090 frame: 1

FLWVQSQPNKSAVKNTNYKVFNVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLGQVQGTMSSEYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNNDNSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKKSE

SEQ ID NO. 8513

STRAIN A909 frame: 1

FLWVQSQPNKSAVKNTNYKVFNVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GGAQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLGQVQGTMSSEYDLANVKKDQSVKIKSKVYPDK
 EWEGKISYISNYPEAEANNNDNSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVNGDKH
 LIVPTSSVTNKNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKKSEV

SEQ ID NO. 8514

STRAIN H36B frame: 1

FLWVQSQPNKSAVKNTNYKVFNVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLGQVQGTMSSEYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNNDNSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVNGDKH
 LIVPTSSVTNKNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 AFKDGQKIDNIESIDLNSNKKSEV

SEQUENCE LISTING

SEQ ID NO. 8515

STRAIN 18RS21 frame: 1

FLWVQSQPKNKSAVKTNKYKVFENVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDNSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSE

SEQ ID NO. 8516

STRAIN M732 frame: 1

FLWVQSQPKNKSAVKTNKYKVFENVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDNSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSEV

SEQ ID NO. 8517

STRAIN COH1 frame: 1

FLWVQSQPKNKSAVKTNKYKVFENVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDNSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSEV

SEQ ID NO. 8518

STRAIN M781 frame: 1

FLWVQSQPKNKSAVKTNKYKVFENVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDNSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSEV

SEQ ID NO. 8519

STRAIN M781 frame: 1

FLWVQSQPKNKSAVKTNKYKVFENVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDNSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSEV

SEQ ID NO. 8520

STRAIN CJB110 frame: 1

FLWVQSQPKNKSAVKTNKYKVFENVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDNSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSEV

SEQ ID NO. 8521

STRAIN 1169NT frame: 1

FLWVQSQPKNKSAVKTNKYKVFENVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK

SEQUENCE LISTING

VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSYDLANVKKDQAVKIKSKVYDPK
EWEGKISYISINYPEAEANNNDNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVINKDNKHFWVYNDNKRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSEV

SEQ ID NO. 8522

STRAIN JM9130013 frame: 1

FLWVQSQPNKSAVKTNKYKVFNVREGSVSSSTLLTGKAKANQEQQVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
GQGAQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSYDLANVKKDQSVKIKSKVYDPK
EWEGKISYISINYPEAEANNNDNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVTNKDNKHFWVYNDNKRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLKSNKKSEVK

SEQ ID NO. 8601

STRAIN 2603

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SEQ ID NO. 8602

STRAIN 090

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AGAAGCTAATCAGTGGGTTAGCCAATGGAAAACTAAACTCTCGCTGCCA
AAAAAGATTACACCATATCTTAAAGCCTAACACTACTTTTACTATTATG
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tGGGAGAACTAATCTATGATTCACTAGGTTATGCTGCCCAgAAAAAGTCA
AAAAAgATGTcTTTAAAAAAGGGTGGTTTACC GTTTCgCAAGAAGCAATC
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AAAAGCAGCTTCatcACTTAAAGAAAGTGATGCTGGAAGAATTTACCAG
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SEQ ID NO. 8603

STRAIN A909

GAAGGCTTCACCTATTATGGAAAAATTCCTG
AAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACACTGGATATTTA
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TAgCCCCGTTTTTGGTAAaCAACTGAAAGGAGCTAAAAAATTAAGTCTG
ATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAaTCATGGTTTTT
GATCAAGATCCAAACATCAATACTCTGAAAAAAATTCACCAACTTTAGT
TATTAAATATGGTGACAAAAATTATTAgATaTGATGCCAGCTTTGGGGA

SEQUENCE LISTING

AAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTAGCCAAaTGGA
 ACTAAACTCTCGCTGCCAAAAAGATTTACACCATATCTTAAACCTAA
 CACTACTTTTACCATTATGGATTTTATGATAAAAAATATCTATTTATATG
 GTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTCAGTGGTTAT
 GCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAAGGGTGGTTTAC
 CGTTTCGCAAGAAGCAATCGGTgATTACGTTGGAGATTATGCCCTTGTTA
 ATATAACAAAAAGCACTAAAAAGCAGCTTCATCACTTAAAGAAAGTGAT
 GTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAGAAAGTAA
 CTACGACGTGTTTTATTTCTCTGACCCTcTATCTTTAGAAGCTCAATTAA
 AATCATTTACAAA

SEQ ID NO. 8604

STRAIN H36B

GAAGGCTTCACCTATTATGGAAAA
 ATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACACTGG
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 GGTTTTTGTATCAAgATCCAAACATCAATACTCTGAAAAAAATTGCACCAA
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 TTGGGGAAaAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTAGCCA
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 AGGTTATGCTGCCCCAgAAAAAGTCAAAAAAgATGTCTTTAAAAAAGGGT
 GGTTTACCGTTTCgCAAGAAGCAATCGGTgATTACGTTGGAGATTATGCC
 CTTGTTAATATAAAACAAAACGACTAAAAAGCAGCTTCaTCACTTAAAGA
 AAGTGATGTTTGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAG
 AAAGTAACCTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGAAGCT
 CAATTAATAATCATTTACAAA

SEQ ID NO. 8605

STRAIN 18RS21

GAAGGCTTCACCTATTATGGA
 AAAATTCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACAC
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 TAGAAAAAGATAGCCCCGTTTTTGGTAAACAACTGAAAGAAGCTAAAAAA
 TTAAGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAAT
 CATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCAC
 CACTTTAGTTATTAATATGGTGCACAAAATTATTTAgATaTGATGCCA
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 CCAATGGAAGAACTAAAACCTCTCGCTGTCAAAAAAGATTTACACCATATCT
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 GGTGGTTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
 GCCCTTGTTAATATAAAACAAAACgACTAAAAAGCAGCTTCATCACTTAA
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 GCTCAATTAAAAATCATTTACAAA

SEQ ID NO. 8606

STRAIN M732

GAAGGCTTCACCTATTATGG
 AAAAATTCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACA
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 TCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCA
 CCAACTTTAGTTATTAATATGGTGCACAAAATTATTTAgATATGATGCC
 AGCCTTGGGGAAAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTA
 GCCAATGGAAGAACTAAAACCTCTCGCTGCCAAAAAGATTTACACCATATC
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 CTATTTATATGGTAATAATTTTGGACgCGGtGGAgAACTAATCTATGATT

SEQUENCE LISTING

CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAA
GGGTGGTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
TGCCCTTGTTAATATAAAACAAAACGACTAAAAAGCAGCTTCATCACTTA
AAGAAAGTGATGCTGGAAGAATTACCAGCTGTCAAAAAAGGGCACATC
ATAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGA
AGCTCAATTAAATCATTTACAAA

SEQ ID NO. 8607

STRAIN COH1

GAAGGCTTCACCTATTATG

GAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTAC
ACTGGGTATTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTTAga
CTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAA
AATTAAGTCTGATGATACAGAAGCTATTGCCGCACAAAACCTGATTTA
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AAGCTCAATTAAATCATTTACAAA

SEQ ID NO. 8608

STRAIN M781

GAAGGCTTCACCTATTATGG

AAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACA
CTGGGTATTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTTAGAC
TTAgAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAA<
ATTAAGTCTGATGATACAGAAGCTATTGCCGCACAAAACCTGATTTAA
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CCAACTTTAGTTATTAAATATGGTGCACAAAATTATTTAgATATGATGCC
AGCCTTGGGGAAAGTATTTCGGTAAAGAAAAAGAAGCTAATCAGTGGGTTA
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CTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATT
CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAA
GGGTGGTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
TGCCCTTGTTAATATAAAACAAAACGACTAAAAAGCAGCTTCATCACTTA
AAGAAAGTGATGTCTGGAAGAATTACCAGCTGTCAAAAAAGGGCACATC
ATAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGA
AGCTCAATTAAATCATTTACAAA

SEQ ID NO. 8609

STRAIN CJB110

GAAGGCTTCACCTATTATGGA

AAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACAC
TGGGTATTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACT
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TTAAGTCTGATGATACAGAAGCTATTGCCGCACAAAACCTGATTTAAT
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CAACTTTAGTTATTAATATGGTGCACAAAATTATTTAgATATGATGCCA
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GGTGGTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
GCCCTTGTTAATATAAAACAAAACGACTAAAAAGCAGCTTCATCACTTAA
AGAAAGTGATGTCTGGAAGAATTACCAGCTGTCAAAAAAGGGCACATCA

SEQUENCE LISTING

TAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGAA
GCTCAATTAAAAATCATTTACAAA

SEQ ID NO. 8610

STRAIN 1169NT

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CCTGAAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACACTGGGTA
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GCTGATGATACAGAAGCTATTGCCGcACAAaaACCTGATTTAATCATGGT
TTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCACCAACTT
TAGTTATTAAATATGGTGCACAAAATTATTTAgATATGATGCCAGCCTTG
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GTTAATATAAAACAAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAG
TGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAGAAA
GTAACCTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGAAGCTCAA
TTAAATCATTTACAAA

SEQ ID NO. 8611

STRAIN JM9130013

GAAGGCTTCACCTATTATG
GAAAAATTCCTGAAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTAC
ACTGGATATTATTAAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGA
CTTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGGAGCTAAAA
AATTAACCTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTA
ATCATGGTTTTTTGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGC
ACCAACTTTAGTTATTAAATATGGTGCACAAAATTATTTAgATATGATGC
CAGCTTTGGGGAAAGTATTTCGGTAAGAAAAAGAAGCTAATCAGTGGGTT
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TCACTAGGTTATGCTGCCCCAgAAAAAGTCAAAAAAGATGTCTTTAAAAA
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AAAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACAT
CATAGAAAGTAACCTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAG
AAGCTCAATTAAATCATTTACAAA

SEQ ID NO. 8612

STRAIN 2603 frame: 1

MKKIGIIVLTLTLFFLVSCGQQTQESTKTTISKMPKIEGFTYYGKIPENPKKVINFTYS
YTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTADDTEAIAAQKPDLMVFDQDPN
INTLKKIAPTLLVIKYGAQNYLDMMPALGKVFGEKEANQWVSQWKTTLAVKKDLHHILK
PNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAPEKVKKDVFKKGWFTVSQEAIGD
YVG DYALVNINKTTKKAASSLKESDVWKNLPAVKKGHIIESNYDVFFYFSDPLSLEAQLKS
FTKAIENTN

SEQ ID NO. 8613

STRAIN 090 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLT
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMMPALGKVFGEKEAN
QWVSQWKTTLAAKKDLHHILKPNNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVG DYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8614

STRAIN A909 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKGAKKLT
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMMPALGKVFGEKEAN

SEQUENCE LISTING

QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVG DYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8615

STRAIN H36B frame: 1

EGFTYYGKIPENPKKVINFYTSYTG YLLKLGVNVSSYSLDLEKDSPVFGKQLKGAKKLT
A
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGEKEAN
QWVSQWKTKTLAAKKDLHHILRPNTTFTIIDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVG DYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8616

STRAIN 18RS21 frame: 1

EGFTYYGKIPENPKKVINFYTSYTG YLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLT
A
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGEKEAN
QWVSQWKTKTLAVKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVG DYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8617

STRAIN M732 frame: 1

EGFTYYGKIPENPKKVINFYTSYTG YLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLT
A
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVG DYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8618

STRAIN COH1 frame: 1

EGFTYYGKIPENPKKVINFYTSYTG YLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLT
A
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVG DYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8619

STRAIN M781 frame: 1

EGFTYYGKIPENPKKVINFYTSYTG YLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLT
A
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVG DYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8620

STRAIN CJB110 frame: 1

EGFTYYGKIPENPKKVINFYTSYTG YLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLT
A
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVG DYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8621

STRAIN 1169NT frame: 1

EGFTYYGKIPENPKKVINFYTSYTG YLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLT
A
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVG DYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8622

STRAIN JM9130013 frame: 1

EGFTYYGKIPENPKKVINFYTSYTG YLLKLGVNVSSYSLDLEKDSPVFGKQLKGAKKLT
A
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGEKEAN

SEQUENCE LISTING

QWVSQWKTKTLAAKKDLHHILKPNNTTFTIMDFYDKNLYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8701

STRAIN 2603

ATGAAATTATCGAAGAAGTTATTGTTTTCGGCTGCTGTT
 TTAACAATGGTGGCGGGTCAACTGTTGAACCAAGTAGCTCAGTTTGCGACTGGAATGAGT
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 AAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTAATGGTGGTATCGAGAATAAA
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 ACAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAGTCTA
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 TATGCAGTTGATGCGAATGCAGAGGGTACAGCAGTAACTTACAAATTAAAAGAAACAAAA
 GCACCAGAAGGTTATGTAATCCCTGATAAAGAAATCGAGTTTACAGTATCACAACATCT
 TATAATACAAAACCAACTGACATCACGGTTGATAGTGTGATGCAACACCTGATACAATT
 AAAAAACAACACGTCCTTCAATCCCTAATACTGGTGGTATTGGTACGGCTATCTTTGTC
 GCTATCGGTGCTGCGGTGATGGCTTTTGCTGTTAAGGGGATGAAGCGTCGTACAAAAGAT
 AAC

SEQ ID NO. 8702

STRAIN 090

GCAGAAGTGTCAACAAGACGCCAGCGAAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
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 GTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTTACCC
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 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAAAAATCA
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 ATTTAAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTTGTTAAAAATC
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 ACAATCCAAAACCATCTAATCCTCCAAGAAAACAGAAAGTTTCACTAGGT
 GGGAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGG
 TGCTGAGTTTGATTTGTGGCTTCTGATGGGACAGCAGTAAATGGACAG
 ATGCTCTTATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCT
 GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
 GATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAG

SEQUENCE LISTING

TAACCTTACAAATTTAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCT
GATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACC
AACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTTAAA
ACAACAAACGTCCTTCA

SEQ ID NO. 8703

STRAIN A909

GCAGAAGTGTCACAAGAACGCCAGCGAA
AACACAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAA
TTACTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAAC
TATGCTAAACTTGGTGACAATGTAAAGGTTTGCAAGGTGTACAGTTTAA
ACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGA
CAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGT
GTCAGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCT
GGATTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATT
CACCTTCAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTA
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ATCAAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTT
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AGCAATTGAAAATTAATTTTGAACCTCAATATGACCATACTCCTGATAAAG
CTGACAATCCAAAACCATCTAATCCTCCAAGAAAACAGAAAGTTCATACT
GGTGGGAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGG
TGGTGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGA
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TGAGATTAAAGGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAG
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AAAACAACAA

SEQ ID NO. 8704

STRAIN 18RS21

GCAGAAGTGTCACAAGAACGCCAGCGAAAAAC
AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
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AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGA
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TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAAT
TACTGATAAAATTTGCAGATGGCTTGACTTATAAATCTGTTGAAAAATCA
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ACAATCCAAAACCATCTAATCCTCCAAGAAAACAGAAAGTTCATACTGGT
GGGAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGG
TGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAG
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SEQUENCE LISTING

GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
GATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGTACAGCAG
TAACTTACAAATTAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCT
GATAAAGAAATCGAGTTTACAGTATCACAACATCTTATAATACAAAACC
AACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAAAA
ACAACAAACGTCCTTCA

SEQ ID NO. 8705

STRAIN M732

GCAGAAGTGTCACAAGAACGCCCAGCGAAAACAACAGT
AAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTA
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ACAAATTAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCTGATAAA
GAAATCGAGTTTACAGTATCACAACATCTTATAATACAAAACCAACTGA
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AACGTCCTTCA

SEQ ID NO. 8706

STRAIN COH1

GCAGAAGTGTCACAAGAACGCCCAGCGAAAAC
AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
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GCTAAACTTGGTGACAATGTAAAAGGTTTGAAGGTGTACAGTTTAAACG
TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
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AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGA
TTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCAC
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ACAATCCAAAACCACTAATCCTCCAAGAAAACAGAAAGTTTCACTAGGTG
GGGAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGG

SEQUENCE LISTING

TGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAG
 ATGCTCTTATTAAAGCGAATACTAATAAAAACTATATGCTGGAGAAGCT
 GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
 GATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAG
 TAACTTACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCACAACATCTTATAATACAAAACC
 AACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAAAA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8707

STRAIN M781

GCAGAAGTGTCAACAAGAACGCCAGCGAAAACAG
 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT
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 TAAACTTGGTGACAATGTAAAGGTTTGCAGGTGTACAGTTTAAACGTT
 ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACA
 GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAG
 TCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATT
 CAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTAAAGAATTACCTT
 TCAAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCACT
 TGCTAACTCTACAGGTACAGGTTTCCCTTCTGaAATTAATATTTACCCTA
 AAAACGTTGTAAGTATGAACCAAAAAACAGATAAAGATGTTAAAAAATTA
 GGTGAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTCTT
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 GATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTGGGA
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SEQ ID NO. 8708

STRAIN CJB110

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 TATGCTAAACTTGGTGACAATGTAAAGGTTTGCAGGTGTACAGTTTAA
 ACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGA
 CAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGT
 GTCAGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCT
 GGATTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATT
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 AGCAATTGAAAATACTTTTGAACCTTCAATATGACCATACTCCTGATAAAG

SEQUENCE LISTING

CTGACAATcCAAAACCATCTAATCCTCCAAGAAAACCAGAAGTTCATACT
GGTGGGAAACGATTGTAAAGAAAGACTCAACAGAAACACAAACACTAGG
TGGTGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGA
CAGATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAA
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CCTGATAAAGAAATCGAGTTTACAGTATCACAACATCTTATAATCCAAA
ACCAACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTA
AAAACAACAAACGTCCTTCA

SEQ ID NO. 8709

STRAIN JM9130013

GCAGAAGTGTCACAAGAACGCCCAGCGAAAACAGCAGTA
AATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTAA
TGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGCTAAAC
TTGGTGACAATGTAAAAGGTTTGCAGGTGTACAGTTTAAACGTTATAAAA
GTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACAGTTGA
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CTCAAAAACTAATGCTCAAGGTTTGGTTCGTCGATGCTCTGGATTCAAAA
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AAATCGAGTTTACAGTATCACAACATCTTATAATACAAAACCACTGAC
ATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAACAAACAA
ACGTCCTTCA

SEQ ID NO. 8710

STRAIN 2603 frame: 1

MKLSKKLLFSAAVLTMVAGSTVEPVAQFATGMSIVRAAEVVSQERPAKTTVNIYKLQADSY
KSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFKRYKVKTDISVDELKKLTVEAAD
AKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLYVEDLKNSPSNITKAYAVPFVLEL
PVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQDDAGYTI GEEFKWFLKSTIPANL
GDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHYTIDEPTVDNQNTLKITFKPEKFK
ETAEELLKGMTLVKNQDALDKATANTDDAAFLIIPVASTINEKAVLGKAIENFELQYDHT
PDKADNPKNPNPRKPEVHTGGKR FVKKDSTETQTLGGA EFDLLASDGTAVKWT DALIKA
NTNKNYIAGEAVTGQPIKLSHTDGT FEIKGLAYAVDANAEGTAVTYKLKETKAPEGYVI
PDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNKRPSIPNTGGIGTAIFVAIGAAM
AFVKGMRRTKDN

SEQ ID NO. 8711

STRAIN 090 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKETAEELLKGMTLVKNQDALDKATANTDDAAFLIIPVAST

SEQUENCE LISTING

TINEKAVLGKAIENFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8712

STRAIN 18RS21 frame: 1

AEVSQERPAKTAVNIYKQLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVK.LGQ
 DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8713

STRAIN M732 frame: 1

AEVSQERPAKTAVNIYKQLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
 DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8714

STRAIN M781 frame: 1

AEVSQERPAKTAVNIYKQLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
 DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 R

SEQ ID NO. 8715

STRAIN COH1 frame: 1

AEVSQERPAKTAVNIYKQLQADSYKSEITXNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
 DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8716

STRAIN CJB110 frame: 1

AEVSQERPAKTAVNIYKQLQADSYKLEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
 DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQUENCE LISTING

SEQ ID NO. 8717

STRAIN JM9130013 frame: 1

AEVSQERPAKTAVNIIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
 VEDLKNSPNSITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
 DDAGYTTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAFFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKCLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8718

STRAIN A909 frame: 1

AEVSQERPAKTTVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
 VEDLKNSPNSITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
 DDAGYTTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAFFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKCLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNN

SEQ ID NO. 8801

STRAIN 2603

ATGCCCTAAGAAGAAATCAGATACCCCGAGAAAAAGAAAGTTGTCTTAACGGAATGGCAA
 AAGCGTAACCTTGAATTTTAAAAAAGCGCAAAGAAGATGAAGAAGACAAAAACGTATT
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 CAAAATACTACTAAAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACCTAATCGCATTAGAAGT
 GCACCTATATTTGTAGTAGCATTCCCTAGTCATTTTAGTTTCCGTTTTCTACTAAGTCCCT
 TTTAGTAAGCAAAAAACAATAACAGTTAGTGGAATCAGCATACACCTGATGATATTTTG
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 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCATATGCACAT
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 ACACAAAATGGTCAGGTTGCGGAAAATAGTCAAGGACAAACAAATAACTCAAATACTAAT
 CAACAAGGACAACAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8802

STRAIN H36B

CCTAAGAAGAAATCAGATACCCCGAGAAAAAGAAAGTT
 GTCTTAACGGAATGGCAAAGCGTAACCTTGAATTTTAAAAAAGCGCAA
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 AAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTACT
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 AAAACGATTATTTCTTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
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 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAAGCTGGAAGAAAG
 GCTGATCCTGTAAATAGTTTCAAGCTACCAAAGCACTTCTTAACAATTA
 CCTTGATAAGGAAGTAGTATTAAGCTATTAATTAAGATTAAAGGCTT
 TAGACCTGATTTAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATTCT

SEQUENCE LISTING

AAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTAT
TAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACAAA
TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
TACACAACAACAAATACCATTGAATCAACCCCTGTTAAAGCAGAAGATAC
AAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGCGG
AAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACAA
CAGATAGCAACAGAGCAGGCACCTAACCTCAAATGTTAAT

SEQ ID NO. 8803

STRAIN 18RS21

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAGTT
GTCTTAACGGAATGGCAAAGCGTAACCTTGAATTTTTAAAAAACGCAA
AGAAGATGAAGAAGAACAAAAACGTATTAACGAAAAATTACGCTTAGATA
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AATCAGCATACACCTGATGATATTTTGATAGAGAAAAAGAAATATTCAA
AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
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GCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATTAA
CCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAGATTAAAGGCTT
TAGCCCTGATTTTAAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATTCT
AAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTAT
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SEQ ID NO. 8804

STRAIN M732

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAG
TTGTCTTAACGGAATGGCAAAGCGTAACCTTGAATTTTTAAAAAACGCG
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CTAAAATTAAGAAGCTTCATTTTCAAAGATTTCAAACCTAAGATTGAA
AAGAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAATAATCG
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CCGTTTTCTACTAATCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCA
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AACAGATAGCAACAGAGCAGGCACCCAACCTCAAATGTTAAT

SEQ ID NO. 8805

STRAIN COH1

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAGTT
GTCTTAACGGAATGGCAAAGCGTAACCTTGAATTTTTAAAAAACGCAA

SEQUENCE LISTING

AGAAGATGAAGAAGAACAAAAACGTATTAACGAAAAATTACGCTTAGATA
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AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAAACCTAAGATTGAAAA
GAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACATAATCGCA
TTAGAAGCTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTTCC
GTTTTCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
AAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCAA
AAAACGATTATTTCTTTTCTTAATTTTAAACATAAAGCTATTGAACAA
CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
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CCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTTAAAGGCTT
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TACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATAC
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SEQ ID NO. 8806

STRAIN M781

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AATTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
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GGAAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGAC
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SEQ ID NO. 8807

STRAIN CJB110

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAG
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ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAAGCTGGAAAA
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SEQUENCE LISTING

AACCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAGATTTAAAGGC
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 CTAACACGACACCTGACCTCCTGCTGTTAGATATGCATGATGGAAATAGT
 ATTAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACA
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 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
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SEQ ID NO. 8808

STRAIN 1169NT

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAGT
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 CGTTTTCTACTAAGTCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGTG
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 GGCTGATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTA
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SEQ ID NO. 8809

STRAIN JM9130013

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAGT
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SEQ ID NO. 8810

STRAIN A909

SEQUENCE LISTING

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAGTTGTC
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 GATCCTGTAAATAGTTTCAAGCTACCAAGCACTTCTTAACAATTAACCT
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 ACCCTGATTTAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATTCTAAA
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 AATACCATTATCTAAATTTAAAGAAAGACTTCTTTTTACAAACAAATTA
 AGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTAC
 ACAACAACAAATACCATTGAATCAACCCCTGTTAAAGCAGAAGATACAAA
 AAATAAATCAACTGATAAAACACAaACAAAATGGTCAGGTTGCGGAAA
 ATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACAACAG
 ATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8811

STRAIN 090

TAAGAAGAAATCAGATACCCAGAAAAAGAAGAAGTTGCTTAACGGAAT
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 AAATATTTCTTCTCTCTGAAGAACCTCAAATACTACTAAAATTAAGAAGC
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 TATATTTGTAGTAGCATTCTAGTCATTTTAGTTTCCGTTTTCTACTAA
 CTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGGAATCAGCATACA
 CCTGATGATATTTTATAGAAAAAACGAATATTCAAAAAAACGATTATTT
 CTTTTCTTTAATTTTTAAACATAAAGCTATTGAACACGTTTAGCTGCAG
 AAGATGTATGGGTAAAAACAGCTCAGATGACTTATCAATTTCCCAATAAG
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 TCTAAATTTAAAGAAAGACTTCTTTTTACAAACAAATTAAGAAGAACCT
 TAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAACAA
 GTACTATTGAATCAACCCCTGTGAAAGCGGAAGATACAAAAAATAAATCA
 ACTGATAAAACACAAACACAAAATGGTCAGGTTGCGGAAAATAGTCAAGG
 ACAAACAATAACTCAAATACTAATCAACAAGGACAACAGATAGCAACAG
 AGCAGGCACCCAAACCTCAAAATGTTAAT

SEQ ID NO. 8812

STRAIN 2603 frame: 1

PKKSDTPEKEEVLTETWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
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 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKLIAYAHTKQYQPVLETGKKADPVNSSELPHKFLTINLDKEDSIKLL
 IKDLKALDPLDISEIQVISLADSKTTPDLLLMDHGDNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTNTIESTFVKAEDTKNKSTDKTQTQNGQVAENSQGTNNSTNTQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8813

STRAIN H36B frame: 1

PKKSDTPEKEEVLTETWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTKIKKHLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF

SEQUENCE LISTING

SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPLDISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPPFYKQIKKN
 LKEPSIVDMEVGVTNTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8814

STRAIN 18RS21 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPLDISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPPFYKQIKKN
 LKEPSIVDMEVGVTNTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8815

STRAIN M732 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPLDISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPPFYKQIKKN
 LKEPSIVDMEVGVTNTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8816

STRAIN COH1 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPLDISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPPFYKQIKKN
 LKEPSIVDMEVGVTNTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8817

STRAIN M781 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPLDISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPPFYKQIKKN
 LKEPSIVDMEVGVTNTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8818

STRAIN CJB110 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPLDISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPPFYKQIKKN
 LKEPSIVDMEVGVTNTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8819

STRAIN 1169NT frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPLDISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPPFYKQIKKN
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SEQUENCE LISTING

QGQQIATEQAPNPQNVN

SEQ ID NO. 8820

STRAIN JM9130013 frame: 1

PKKKS DTP EKEE VVL TEW QKR NLE FLK KR KE D E E E Q K R I N E K L R L D K R S K L N I S S P E E P Q
 N T T K I K K L H F P K I S R P K I E K K Q K K E I V N S L A K T N R I R T A P I F V V A F L V I L V S V F L L T P F
 S K Q K T I T V S G N Q H T P D D I L I E K T N I Q K N D Y F F S L I F K H K A I E Q R L A A E D V W V K T A Q M T Y Q
 F P N K F H I Q V Q E N K I I A Y A H T K Q G Y Q P V L E T G K K A D P V N S S E L P K H F L T I N L D K E D S I K L L
 I K D L K A L D P D L I S E I Q V I S L A D S K T T P D L L L L D M H D G N S I R I P L S K F K E R L P F Y K Q I K K N
 L K E P S I V D M E V G V Y T T T N T I E S T P V K A E D T K N K S T D K T Q T Q N G Q V A E N S Q G Q T N N S N T N Q
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8821

STRAIN A909 frame: 1

PKKKS DTP EKEE VVL TEW QKR NLE FLK KR KE D E E E Q K R I N E K L R L D K R S K L N I S S P E E P Q
 N T T K I K K L H F P K I S R P K I E K K Q K K E I V N S L A K T N R I R T A P I F V V A F L V I L V S V F L L T P F
 S K Q K T I T V S G N Q H T P D D I L I E K T N I Q K N D Y F F S L I F K H K A I E Q R L A A E D V W V K T A Q M T Y Q
 F P N K F H I Q V Q E N K I I A Y A H T K Q G Y Q P V L E T G K K A D P V N S S E L P K H F L T I N L D K E D S I K L L
 I K D L K A L D P D L I S E I Q V I S L A D S K T T P D L L L L D M H D G N S I X I P L S K F K E R L P F Y K Q I K K N
 L K E P S I V D M E V G V Y T T T N T I E S T P V K A E D T K N K S T D K T Q X Q N G Q V A E N S Q G Q T N N S N T N Q
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8822

STRAIN 090 frame: 2

KKKSDTP EKEE VVL TEW QKR NLE FLK KR KE D E E E Q K R I N E K L R L D K R S K L N I S S P E E P Q N
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 K Q K T I T V S G N Q H T P D D I L I E K T N I Q K N D Y F F S L I F K H K A I E Q R L A A E D V W V K T A Q M T Y Q F
 P N K F H I Q V Q E N K I I A Y A H T K Q G Y Q P V L E T G K K A D P V N S S E L P K H F L T I N L D K E D S I K L L I
 K D L K A L D P D L I S E I Q V I S L A D S K T T P D L L L L D M H D G N S I R I P L S K F K E R L P F Y K Q I K K N L
 K E P S I V D M E V G V Y T T T S T I E S T P V K A E D T K N K S T D K T Q T Q N G Q V A E N S Q G Q T N N S N T N Q Q
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SEQ ID NO. 8901

STRAIN 2603

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SEQ ID NO. 8902

SEQUENCE LISTING

STRAIN 090

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SEQ ID NO. 8903

STRAIN A909

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SEQUENCE LISTING

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SEQ ID NO. 8904

STRAIN H3B6

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SEQ ID NO. 8905

STRAIN 18RS21

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SEQUENCE LISTING

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SEQ ID NO. 8906

STRAIN M732

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SEQ ID NO. 8907

STRAIN COH1

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SEQUENCE LISTING

CTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATCAAGAGAAA
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SEQ ID NO. 8908

STRAIN M781

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SEQ ID NO. 8909

STRAIN CJB110

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SEQUENCE LISTING

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 GTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTA
 CCTAAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAGAGTCA
 ACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAAAA
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 AAGAGTTATTCGGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8910

STRAIN 1169NT

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 AAGTCCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCTG
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 GTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGGTGG
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 CAACCTAAAGTATCAAGTCCAGTGAATTTAATTTTCAAAGGGTGAAAA

SEQUENCE LISTING

AATACATTATGATCAAGTGTTAGTAGTAGATGGTCATCAGTGGATTTCAT
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SEQ ID NO. 8911

STRAIN JM9130013

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TCAACCTAAAGTATCAAGTCCAGTGGAATTTAATTTTCAAAGGGTGAAA
AAATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTCA
TACAAGAGTTATTCCGGTATTTCGTCGCTATATTGAAATT

SEQ ID NO. 8912

STRAIN 2603 frame: 1

MKKQVNDTKQSYSLRKYKFLASVILGSFIMVTSFVFADQTTSVQVNNQTGTSVDANNSS
SNETSASSVITSNNDVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKE
TEVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVWISYKSFQVRRYAAIESLDPSSGGS
ETKAPTPTVNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILT
IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGTF
DILITNLIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKVAVSFADHKNEKGLYN
IHLYYQEASGTLVGVGTGKVTVAGTNSQEPINGLAKTGNYNIIGSTEVKNEAKISSQT
QFTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTSSEKAKDEATKPTSYFN
LPKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRY
IEI

SEQ ID NO. 8913

STRAIN 090 frame: 1

MKKQVNDTKQSYSLRKYKFLASVILGSFIMVTSFVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKE
EVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVWISYKSFQVRRYAAIESLDPSSGSE
TKAPTPTVNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILT
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGTF
ILITNLIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKVAVSFADHKNEKGLYN
IHLYYQEASGTLVGVGTGKVTVAGTNSQEPINGLAKTGNYNIIGSTEVKNEAKISSQT
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTSSEKAKDEATKPTSYFN
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRY
EI

SEQUENCE LISTING

SEQ ID NO. 8914

STRAIN A909 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSFVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNVYVSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGSE
 TKAPTPTVNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVTGKTVTAGTNSSQEPiENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8915

STRAIN H36B frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSFVFADQTTSVQVNNQTGTSVDNNSS
 NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNVYVSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGSE
 TKAPTPTVNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
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 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVTGKTVTAGTNSSQEPiENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8916

STRAIN 18RS21 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSFVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNVYVSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGSE
 TKAPTPTVNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVTGKTVTAGTNSSQEPiENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8917

STRAIN M732 frame: 1

QVNDTKQSYSLRKYKFGLASVILGSFIMVTSFVFADQTTSVQVNNQTGTSVDANNSSNET
 SASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNVYVSKETEVK
 NTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFGVRRYAAIESLDPSGGSETKA
 PTPVNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFDILI
 TNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHKNEKGLYNIHLY
 YQEASGTLVGVTGKTVTAGTNSSQEPiENGLPKTGVYNIIGSTEVKNEAKISSQTQFTL
 EKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHQWISYKSYSGIRRYIEI

SEQ ID NO. 8918

STRAIN COH1 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSFVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNVYVSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFGVRRYAAIESLDPSGGSE
 TKAPTPTVNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVTGKTVTAGTNSSQEPiENGLPKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQUENCE LISTING

SEQ ID NO. 8919

STRAIN M781 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSFVFADQTTSVQVNNQTGTSVDANNSS
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 EVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVWKWISYKSFQGVRRYAAIESLDPGGSE
 TKAPTPTVNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDNKYKAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVTGTKVTAGTNSSQEPINGLPKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8920

STRAIN CJB110 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSFVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
 EVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVWKWISYKSFQGVRRYAAIESLDPGGSE
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 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDNKYKAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVTGTKVTAGTNSSQEPINGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8921

STRAIN 1169NT frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSFVFADQTTSVQVNNQTGTSVDANNSS
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 EVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVWKWISYKSFQGVRRYAAIESLDPGGSE
 TKAPTPTVNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDNKYKAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVTGTKVTAGTNSSQEPINGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8922

STRAIN JM9130013 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSFVFADQTTSVQVNNQTGTSVDANNSS
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 EVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVWKWISYKSFQGVRRYAAIESLDPGGSE
 TKAPTPTVNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTINETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDNKYKAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVTGTKVTAGTNSSQEPINGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHWISYKSYSGIRRYI
 EI

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0001	453	chromosomal replication initiator protein DnaA
SAG0002	378	DNA polymerase III, beta subunit
SAG0003	293	diacylglycerol kinase catalytic domain protein, putative
SAG0004	65	conserved hypothetical protein
SAG0005	67	hypothetical protein
SAG0006	371	GTP-binding protein YchF
SAG0007	191	peptidyl-tRNA hydrolase
SAG0008	1165	transcription-repair coupling factor
SAG0009	31	hypothetical protein
SAG0010	90	S4 domain protein
SAG0011	123	cell division protein DivIC, putative
SAG0012	44	conserved hypothetical protein
SAG0013	428	protein of unknown function
SAG0014	424	MesJ/Ycf62 family protein
SAG0015	180	hypoxanthine-guanine phosphoribosyltransferase
SAG0016	658	cell division protein FtsH
SAG0017	447	pcsB protein
SAG0018	322	ribose-phosphate pyrophosphokinase
SAG0019	391	aminotransferase, class I
SAG0020	253	recombination protein O
SAG0021	283	protease, putative
SAG0022	330	fatty acid/phospholipid synthesis protein PlsX
SAG0023	79	acyl carrier protein
SAG0024	234	phosphoribosylaminoimidazole-succinocarboxamide synthase
SAG0025	1241	phosphoribosylformylglycinamide synthase, putative
SAG0026	484	amidophosphoribosyltransferase
SAG0027	340	phosphoribosylformylglycinamide cyclo-ligase
SAG0028	182	phosphoribosylglycinamide formyltransferase
SAG0029	250	acetyltransferase, GNAT family
SAG0030	515	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
SAG0031	299	peptidase, M23/M37 family
SAG0032	434	group B streptococcal surface immunogenic protein
SAG0033	232	N-acetylmannosamine-6-P epimerase, putative
SAG0034	438	sugar ABC transporter, sugar-binding protein
SAG0035	295	sugar ABC transporter, permease protein
SAG0036	276	sugar ABC transporter, permease protein
SAG0037	147	conserved hypothetical protein
SAG0038	220	conserved hypothetical protein
SAG0039	305	N-acetylneuraminate lyase, putative
SAG0040	293	ROK family protein
SAG0041	325	acetyl xylan esterase, putative
SAG0042	267	phosphosugar-binding transcriptional regulator, RpiR family, putative
SAG0043	421	phosphoribosylamine--glycine ligase
SAG0044	162	phosphoribosylaminoimidazole carboxylase, catalytic subunit
SAG0045	363	phosphoribosylaminoimidazole carboxylase, ATPase subunit
SAG0046	463	membrane protein, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0047	432	adenylosuccinate lyase
SAG0048	303	transcriptional regulator, Cro/CI family
SAG0049	332	Holliday junction DNA helicase RuvB
SAG0050	145	phosphotyrosine protein phosphatase, low molecular weight
SAG0051	126	MORN motif family protein
SAG0052	592	membrane protein, putative
SAG0053	880	aldehyde-alcohol dehydrogenase
SAG0054	338	alcohol dehydrogenase, propanol-preferring
SAG0055	496	threonine synthase
SAG0056	412	MATE efflux family protein
SAG0057	102	ribosomal protein S10
SAG0058	208	ribosomal protein L3
SAG0059	207	ribosomal protein L4
SAG0060	98	ribosomal protein L23
SAG0061	277	ribosomal protein L2
SAG0062	92	ribosomal protein S19
SAG0063	114	ribosomal protein L22
SAG0064	217	ribosomal protein S3
SAG0065	137	ribosomal protein L16
SAG0066	68	ribosomal protein L29
SAG0067	86	ribosomal protein S17
SAG0068	122	ribosomal protein L14
SAG0069	101	ribosomal protein L24
SAG0070	180	ribosomal protein L5
SAG0071	61	ribosomal protein S14, putative
SAG0072	132	ribosomal protein S8
SAG0073	178	ribosomal protein L6
SAG0074	118	ribosomal protein L18
SAG0075	164	ribosomal protein S5
SAG0076	59	ribosomal protein L30
SAG0077	146	ribosomal protein L15
SAG0078	434	preprotein translocase, SecY subunit
SAG0079	212	adenylate kinase
SAG0080	72	translation initiation factor IF-1
SAG0081	38	ribosomal protein L36
SAG0082	121	ribosomal protein S13
SAG0083	118	ribosomal protein S11
SAG0084	312	DNA-directed RNA polymerase, alpha subunit
SAG0085	128	ribosomal protein L17
SAG0086	85	lipoprotein, putative
SAG0087	59	hypothetical protein
SAG0088	56	hypothetical protein
SAG0089	183	conserved hypothetical protein
SAG0090	139	conserved hypothetical protein
SAG0091	144	transcriptional regulator ComX1, putative
SAG0092	230	phosphoglycerate mutase family protein
SAG0093	250	D-alanyl-D-alanine carboxypeptidase family protein
SAG0094	191	N-acetylmuramoyl-L-alanine amidase, family 4 protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0095	344	heat-inducible transcription repressor HrcA
SAG0096	190	heat shock protein GrpE
SAG0097	609	dnaK protein
SAG0098	379	dnaJ protein
SAG0099	415	transcriptional regulator, GntR family
SAG0100	258	tRNA pseudouridine synthase A
SAG0101	252	phosphomethylpyrimidine kinase, putative
SAG0102	154	conserved hypothetical protein
SAG0103	189	conserved hypothetical protein TIGR01440
SAG0104	280	conserved hypothetical protein
SAG0105	427	trigger factor
SAG0106	191	DNA-directed RNA polymerase, delta subunit, putative
SAG0107	534	CTP synthase
SAG0108	308	conserved hypothetical protein
SAG0109	148	deoxyuridine 5'-triphosphate nucleotidohydrolase
SAG0110	454	DNA repair protein RadA
SAG0111	165	carbonic anhydrase-related protein
SAG0112	439	pyridine nucleotide-disulphide oxidoreductase family protein
SAG0113	484	glutamyl-tRNA synthetase
SAG0114	322	ribose ABC transporter, periplasmic D-ribose-binding protein
SAG0115	310	ribose ABC transporter, permease protein
SAG0116	492	ribose ABC transporter, ATP-binding protein
SAG0117	132	ribose ABC transporter protein RbsD
SAG0118	303	ribokinase
SAG0119	328	ribose operon repressor RbsR
SAG0120	32	hypothetical protein
SAG0121	362	permease, putative
SAG0122	228	ABC transporter, ATP-binding protein
SAG0123	223	DNA-binding response regulator
SAG0124	356	sensor histidine kinase
SAG0125	396	argininosuccinate synthase
SAG0126	462	argininosuccinate lyase
SAG0127	293	fructose-bisphosphate aldolase
SAG0128	305	L-2-hydroxyisocaproate dehydrogenase
SAG0129	62	ribosomal protein L28
SAG0130	121	conserved hypothetical protein
SAG0131	543	DAK2 domain protein
SAG0132	294	SPFH domain/Band 7 family protein
SAG0133	38	conserved hypothetical protein
SAG0134	96	hypothetical protein
SAG0135	246	amino acid ABC transporter, ATP-binding protein
SAG0136	516	amino acid ABC transporter, amino acid-binding protein/permease protein
SAG0137	627	conserved hypothetical protein
SAG0138	279	undecaprenol kinase, putative
SAG0139	251	negative regulator of competence MecA, putative
SAG0140	386	glycosyl transferase, group 4 family protein
SAG0141	256	ABC transporter, ATP-binding protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0142	420	conserved hypothetical protein
SAG0143	410	selenocysteine lyase
SAG0144	147	NifU family protein
SAG0145	472	conserved hypothetical protein
SAG0146	395	penicillin-binding protein 4, putative
SAG0147	411	D-alanyl-D-alanine carboxypeptidase family protein
SAG0148	551	oligopeptide ABC transporter, substrate-binding protein, putative
SAG0149	304	oligopeptide ABC transporter, permease protein
SAG0150	343	oligopeptide ABC transporter, permease protein
SAG0151	348	oligopeptide ABC transporter, ATP-binding protein
SAG0152	310	oligopeptide ABC transporter, ATP-binding protein
SAG0153	283	4-diphosphocytidyl-2C-methyl-D-erythritol kinase
SAG0154	147	adc operon repressor AdcR
SAG0155	236	zinc ABC transporter, ATP-binding protein
SAG0156	270	zinc ABC transporter, permease protein
SAG0157	NA	deoxyribonuclease-related protein, degenerate
SAG0158	419	tyrosyl-tRNA synthetase
SAG0159	765	penicillin-binding protein 1B, putative
SAG0160	1191	DNA-directed RNA polymerase, beta subunit
SAG0161	1216	DNA-directed RNA polymerase beta' subunit
SAG0162	121	conserved hypothetical protein
SAG0163	323	competence protein CglA
SAG0164	282	competence protein CglB
SAG0165	151	conserved hypothetical protein
SAG0166	123	conserved domain protein
SAG0167	324	conserved hypothetical protein
SAG0168	397	acetate kinase
SAG0169	68	transcriptional regulator, Cro/CI family
SAG0170	45	hypothetical protein
SAG0171	151	hypothetical protein
SAG0172	221	protease, putative
SAG0173	256	pyrroline-5-carboxylate reductase
SAG0174	355	glutamyl-aminopeptidase
SAG0175	79	hypothetical protein
SAG0176	94	conserved hypothetical protein
SAG0177	107	thioredoxin family protein
SAG0178	208	tRNA binding domain protein
SAG0179	238	conserved hypothetical protein
SAG0180	131	single-strand binding protein
SAG0181	214	hydrolase, haloacid dehalogenase-like family
SAG0182	581	sensor histidine kinase, putative
SAG0183	246	response regulator
SAG0184	151	conserved hypothetical protein
SAG0185	242	membrane protein, putative
SAG0186	36	hypothetical protein
SAG0187	542	oligopeptide ABC transporter, oligopeptide-binding protein
SAG0188	325	oligopeptide ABC transporter, permease protein
SAG0189	273	oligopeptide ABC transporter, permease protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0190	267	peptide ABC transporter, ATP-binding protein
SAG0191	208	peptide ABC transporter, ATP-binding protein
SAG0192	676	PTS system, IIABC components
SAG0193	541	alpha amylase family protein
SAG0194	639	transcriptional antiterminator, BglG family
SAG0195	377	IS1548, transposase
SAG0196	66	conserved domain protein
SAG0197	94	PTS system, IIB component, putative
SAG0198	451	PTS system, IIC component, putative
SAG0199	285	transketolase, N-terminal subunit
SAG0200	309	transketolase, C-terminal subunit
SAG0201	419	oxidoreductase, putative
SAG0202	89	ribosomal protein S15
SAG0203	709	polysaccharide nucleotidyltransferase
SAG0204	250	conserved hypothetical protein
SAG0205	194	serine O-acetyltransferase
SAG0206	60	lipoprotein, putative
SAG0207	447	cysteinyI-tRNA synthetase
SAG0208	128	conserved hypothetical protein
SAG0209	251	RNA methyltransferase, TrmH family, group 3
SAG0210	172	conserved hypothetical protein
SAG0211	286	DegV family protein
SAG0212	32	hypothetical protein
SAG0213	39	hypothetical protein
SAG0214	148	ribosomal protein L13
SAG0215	130	ribosomal protein S9
SAG0216	33	hypothetical protein
SAG0217	384	site-specific recombinase, phage integrase family
SAG0218	158	transcriptional regulator, Cro/CI family
SAG0219	101	hypothetical protein
SAG0220	92	conserved hypothetical protein
SAG0221	76	hypothetical protein
SAG0222	108	conserved domain protein
SAG0223	209	conserved hypothetical protein, fusion
SAG0224	332	replication initiation protein, putative
SAG0225	144	hypothetical protein
SAG0226	418	recombination protein
SAG0227	156	hypothetical protein
SAG0228	111	conserved hypothetical protein
SAG0229	95	conserved hypothetical protein
SAG0230	96	conserved hypothetical protein
SAG0231	135	hypothetical protein
SAG0232	186	hypothetical protein
SAG0233	226	hypothetical protein
SAG0234	128	hypothetical protein
SAG0235	93	hypothetical protein
SAG0236	32	hypothetical protein
SAG0237	34	hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0238	41	hypothetical protein
SAG0239	286	transcriptional regulator MutR family
SAG0240	393	transporter, putative
SAG0241	213	amino acid ABC transporter, permease protein
SAG0242	308	amino acid ABC transporter, amino acid-binding protein
SAG0243	211	amino acid ABC transporter, permease protein
SAG0244	381	amino acid ABC transporter, ATP-binding protein
SAG0245	152	protein of unknown function/lipoprotein, putative
SAG0246	268	hypothetical protein
SAG0247	116	hypothetical protein
SAG0248	90	hypothetical protein
SAG0249	116	hypothetical protein
SAG0250	193	membrane protein, putative
SAG0251	72	transcriptional regulator, Cro/CI family
SAG0252	186	acetyltransferase, GNAT family
SAG0253	192	acetyltransferase, GNAT family
SAG0254	226	acetyltransferase, GNAT family
SAG0255	315	conserved hypothetical protein
SAG0256	163	RNA polymerase sigma factor, ECF subfamily
SAG0257	53	lipoprotein, putative
SAG0258	202	transcriptional regulator, TetR family
SAG0259	365	ABC transporter efflux protein, DrrB family, putative
SAG0260	238	ABC transporter, ATP-binding protein
SAG0261	129	IS1381, transposase OrfB
SAG0262	127	IS1381, transposase OrfA
SAG0263	171	hypothetical protein
SAG0264	103	conserved hypothetical protein
SAG0265	235	conserved hypothetical protein
SAG0266	382	N-acetylglucosamine-6-phosphate deacetylase
SAG0267	180	conserved hypothetical protein
SAG0268	304	glycyl-tRNA synthetase, alpha subunit
SAG0269	213	acyl carrier protein phosphodiesterase, putative
SAG0270	679	glycyl-tRNA synthetase, beta subunit
SAG0271	85	conserved hypothetical protein
SAG0272	87	membrane protein, putative
SAG0273	502	glycerol kinase
SAG0274	609	alpha-glycerophosphate oxidase
SAG0275	232	glycerol uptake facilitator protein
SAG0276	445	NADH oxidase, putative
SAG0277	476	conserved hypothetical protein
SAG0278	661	transketolase
SAG0279	101	conserved hypothetical protein
SAG0280	244	ABC transporter, ATP-binding protein
SAG0281	534	membrane protein, putative
SAG0282	461	PTS system, IIBC components
SAG0283	267	glutamate 5-kinase
SAG0284	417	gamma-glutamyl phosphate reductase
SAG0285	298	conserved hypothetical protein TIGR00006

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0286	108	cell division protein FtsL, putative
SAG0287	752	penicillin-binding protein 2X
SAG0288	336	phospho-N-acetylmuramoyl-pentapeptide-transferase
SAG0289	447	ATP-dependent RNA helicase, DEAD/DEAH box family
SAG0290	270	ABC transporter, substrate-binding protein
SAG0291	267	amino acid ABC transporter, permease protein
SAG0292	247	amino acid ABC transporter, ATP-binding protein
SAG0293	74	conserved hypothetical protein
SAG0294	304	thioredoxin reductase
SAG0295	486	conserved hypothetical protein
SAG0296	273	NAD synthetase
SAG0297	444	aminopeptidase C
SAG0298	750	penicillin-binding protein 1A
SAG0299	199	recombination protein U
SAG0300	172	conserved hypothetical protein
SAG0301	40	hypothetical protein
SAG0302	110	conserved hypothetical protein
SAG0303	384	conserved hypothetical protein
SAG0304	487	conserved hypothetical protein
SAG0305	160	autoinducer-2 production protein LuxS
SAG0306	535	KH domain protein
SAG0307	33	hypothetical protein
SAG0308	298	ABC transporter, ATP-binding protein
SAG0309	246	ABC transporter, permease protein, putative
SAG0310	361	conserved hypothetical protein
SAG0311	NA	DNA-binding response regulator, authentic point mutation
SAG0312	234	conserved hypothetical protein
SAG0313	209	guanylate kinase
SAG0314	104	DNA-directed RNA polymerase, omega subunit, putative
SAG0315	796	primosomal protein N ⁱ
SAG0316	311	methionyl-tRNA formyltransferase
SAG0317	440	sun protein
SAG0318	245	serine/threonine phosphatase, putative
SAG0319	651	serine/threonine protein kinase
SAG0320	231	conserved hypothetical protein
SAG0321	339	sensor histidine kinase, putative
SAG0322	213	DNA-binding response regulator
SAG0323	466	hydrolase, haloacid dehalogenase family/peptidyl-prolyl cis-trans isomerase, cyclophilin type
SAG0324	124	general stress protein, putative
SAG0325	258	pyruvate formate-lyase-activating enzyme
SAG0326	251	transcriptional regulator, DeoR family
SAG0327	327	transcriptional regulator, putative
SAG0328	107	PTS system, cellobiose-specific IIA component
SAG0329	106	PTS system, cellobiose-specific IIB component
SAG0330	433	PTS system, cellobiose-specific IIC component
SAG0331	818	formate acetyltransferase
SAG0332	222	transaldolase family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0333	362	glycerol dehydrogenase
SAG0334	308	cysteine synthase A
SAG0335	214	conserved hypothetical protein TIGR00257
SAG0336	429	helicase, putative
SAG0337	221	competence protein F, putative
SAG0338	184	ribosomal subunit interface protein
SAG0339	450	aspartate kinase family protein
SAG0340	216	hydrolase, haloacid dehalogenase-like family
SAG0341	49	hypothetical protein
SAG0342	263	enoyl-CoA hydratase/isomerase family protein
SAG0343	144	transcriptional regulator, MarR family
SAG0344	323	3-oxoacyl-(acyl-carrier-protein) synthase III
SAG0345	74	acyl carrier protein
SAG0346	319	enoyl-(acyl-carrier-protein) reductase II
SAG0347	308	malonyl CoA-acyl carrier protein transacylase
SAG0348	244	3-oxoacyl-[acyl-carrier protein] reductase
SAG0349	410	3-oxoacyl-(acyl-carrier-protein) synthase II
SAG0350	166	acetyl-CoA carboxylase, biotin carboxyl carrier protein
SAG0351	140	(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase
SAG0352	456	acetyl-CoA carboxylase, biotin carboxylase
SAG0353	291	acetyl-CoA carboxylase, carboxyl transferase, beta subunit
SAG0354	257	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit
SAG0355	210	conserved hypothetical protein
SAG0356	425	seryl-tRNA synthetase
SAG0357	330	membrane protein, putative
SAG0358	120	conserved hypothetical protein
SAG0359	303	PTS system, mannose-specific IID component
SAG0360	270	PTS system, mannose-specific IIC component
SAG0361	336	PTS system, mannose-specific IIAB components
SAG0362	270	hydrolase, haloacid dehalogenase-like family
SAG0363	194	hypothetical protein
SAG0364	203	membrane protein, putative
SAG0365	473	xanthine/uracil permease family protein
SAG0366	169	conserved hypothetical protein TIGR00150
SAG0367	186	acetyltransferase, GNAT family
SAG0368	435	protein of unknown function
SAG0369	98	conserved hypothetical protein
SAG0370	139	HIT family protein
SAG0371	167	hypothetical protein
SAG0372	85	hypothetical protein
SAG0373	241	ABC transporter, ATP-binding protein
SAG0374	344	ABC transporter, permease protein
SAG0375	266	conserved hypothetical protein
SAG0376	211	conserved hypothetical protein TIGR00091
SAG0377	127	conserved hypothetical protein
SAG0378	379	N utilization substance protein A
SAG0379	98	conserved hypothetical protein
SAG0380	100	ribosomal protein L7A family

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0381	927	translation initiation factor IF-2
SAG0382	122	ribosome-binding factor A
SAG0383	334	protein of unknown function/lipoprotein, putative
SAG0384	138	transcriptional repressor CopY
SAG0385	744	copper-transporter ATPase CopA
SAG0386	68	copper-transporter protein CopZ
SAG0387	204	membrane protein, putative
SAG0388	270	hydrolase, haloacid dehalogenase-like family
SAG0389	880	DNA polymerase I
SAG0390	146	CoA-binding domain protein
SAG0391	159	transcriptional regulator, Fur family
SAG0392	521	cell wall surface anchor family protein
SAG0393	228	DNA-binding response regulator
SAG0394	345	sensor histidine kinase
SAG0395	246	membrane protein, putative
SAG0396	380	queuine tRNA-ribosyltransferase
SAG0397	102	conserved hypothetical protein
SAG0398	179	BioY family protein
SAG0399	258	AtsA/ElaC family protein
SAG0400	168	cytidine/deoxycytidylate deaminase family protein
SAG0401	44	hypothetical protein
SAG0402	449	glucose-6-phosphate isomerase
SAG0403	175	5-formyltetrahydrofolate cyclo-ligase family protein
SAG0404	225	rhomboid family protein
SAG0405	347	protein of unknown function/lipoprotein, putative
SAG0406	299	UTP-glucose-1-phosphate uridylyltransferase
SAG0407	338	glycerol-3-phosphate dehydrogenase (NAD(P)+)
SAG0408	109	ribonuclease P protein component
SAG0409	271	SpoIIJ family protein
SAG0410	273	R3H domain protein
SAG0411	177	conserved hypothetical protein
SAG0412	258	recX protein
SAG0413	451	RNA methyltransferase, TrmA family
SAG0414	153	conserved hypothetical protein
SAG0415	142	acetyltransferase, GNAT family
SAG0416	1233	protease, putative
SAG0417	302	glycosyl transferase, group 2 family protein
SAG0418	336	ribonucleoside-diphosphate reductase 2, beta subunit
SAG0419	137	nrdI protein
SAG0420	721	ribonucleoside-diphosphate reductase 2, alpha subunit
SAG0421	1055	cell wall surface anchor family protein
SAG0422	129	conserved hypothetical protein
SAG0423	132	conserved domain protein
SAG0424	94	hypothetical protein
SAG0425	105	carboxymuconolactone decarboxylase family protein
SAG0426	131	conserved hypothetical protein
SAG0427	129	transcriptional regulator, MerR family
SAG0428	345	alcohol dehydrogenase, zinc-containing

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0429	284	oxidoreductase, aldo/keto reductase family
SAG0430	287	cation efflux system protein
SAG0431	174	transcriptional regulator, TetR family
SAG0432	397	transcriptional regulator, AraC family
SAG0433	1389	surface protein Rib
SAG0434	61	transposase, IS256 family, truncation
SAG0435	97	DNA-damage-inducible protein J, putative
SAG0436	62	hypothetical protein
SAG0437	123	lipoprotein, putative
SAG0438	145	bacteriophage L54a, integrase, truncation
SAG0439	NA	conserved hypothetical protein, degenerate
SAG0440	84	conserved hypothetical protein
SAG0441	103	conserved domain protein
SAG0442	189	acetyltransferase, GNAT family
SAG0443	194	acetyltransferase, GNAT family
SAG0444	188	conserved hypothetical protein
SAG0445	883	valyl-tRNA synthetase
SAG0446	319	oxidoreductase, Gfo/Idh/MocA family
SAG0447	287	magnesium transporter, CorA family
SAG0448	391	transposase, IS256 family
SAG0449	354	conserved hypothetical protein
SAG0450	330	aspartate--ammonia ligase
SAG0451	149	bacteriocin transport accessory protein, putative
SAG0452	179	type II DNA modification methyltransferase, putative
SAG0453	96	hypothetical protein
SAG0454	161	phosphopantetheine adenyltransferase
SAG0455	357	conserved hypothetical protein
SAG0456	NA	conserved hypothetical protein, degenerate
SAG0457	192	conserved hypothetical protein
SAG0458	368	conserved hypothetical protein TIGR00048
SAG0459	171	VanZF domain protein
SAG0460	581	ABC transporter, ATP-binding/permease protein
SAG0461	579	ABC transporter, ATP-binding/permease protein
SAG0462	188	anthranilate synthase component II
SAG0463	179	BioY family protein
SAG0464	330	biotin synthetase
SAG0465	164	hypothetical protein
SAG0466	371	thiolase
SAG0467	409	AMP-binding enzyme domain protein
SAG0468	210	endonuclease III
SAG0469	131	type IV prepilin peptidase-related protein
SAG0470	69	conserved hypothetical protein
SAG0471	322	glucokinase
SAG0472	126	rhodanese-like family protein
SAG0473	613	elongation factor Tu family protein
SAG0474	81	conserved hypothetical protein
SAG0475	451	UDP-N-acetylmuramoylalanine--D-glutamate ligase
SAG0476	358	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
		pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
SAG0477	378	cell division protein DivIB, putative
SAG0478	429	cell division protein FtsA
SAG0479	426	cell division protein FtsZ
SAG0480	224	ylmE protein, putative
SAG0481	201	ylmF protein
SAG0482	84	YGGT family protein
SAG0483	262	ylmH protein
SAG0484	256	cell division protein DivIVA, putative
SAG0485	930	isoleucyl-tRNA synthetase
SAG0486	100	conserved hypothetical protein
SAG0487	151	MutT/nudix family protein
SAG0488	753	ATP-dependent Clp protease, ATP-binding subunit
SAG0489	34	hypothetical protein
SAG0490	76	conserved hypothetical protein
SAG0491	230	amino acid ABC transporter, permease protein
SAG0492	244	amino acid ABC transporter, ATP-binding protein
SAG0493	564	phosphoglucomutase/phosphomannomutase family protein
SAG0494	284	methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase
SAG0495	278	protein of unknown function
SAG0496	446	exodeoxyribonuclease VII, large subunit
SAG0497	71	exodeoxyribonuclease VII, small subunit
SAG0498	290	geranyltranstransferase, putative
SAG0499	275	hemolysin A
SAG0500	157	arginine repressor ArgR, putative
SAG0501	552	DNA repair protein RecN
SAG0502	278	DegV family protein
SAG0503	279	lipase/acylhydrolase
SAG0504	200	conserved hypothetical protein
SAG0505	91	DNA-binding protein HU
SAG0506	65	hypothetical protein
SAG0507	310	dihydroorotate dehydrogenase A
SAG0508	411	beta-lactam resistance factor
SAG0509	403	beta-lactam resistance factor
SAG0510	406	murM protein, putative
SAG0511	270	hydrolase, haloacid dehalogenase-like family
SAG0512	438	HD domain protein
SAG0513	128	conserved hypothetical protein
SAG0514	894	cation-transporting ATPase, E1-E2 family
SAG0515	286	conserved hypothetical protein
SAG0516	643	fructose-1,6-bisphosphatase, putative
SAG0517	374	iron-sulfur cluster-binding protein, putative
SAG0518	NA	peptide chain release factor 2, programmed frameshift
SAG0519	230	cell division ABC transporter, ATP-binding protein FtsE
SAG0520	309	cell division ABC transporter, permease protein FtsX
SAG0521	236	carboxymethylenebutenolidase-related protein
SAG0522	232	metallo-beta-lactamase superfamily protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0523	254	oxidoreductase, short chain dehydrogenase/reductase family
SAG0524	835	DNA polymerase III, epsilon subunit/ATP-dependent helicase DinG
SAG0525	397	aspartate aminotransferase
SAG0526	448	asparaginyl-tRNA synthetase
SAG0527	185	conserved hypothetical protein
SAG0528	327	inosine-uridine preferring nucleoside hydrolase
SAG0529	38	hypothetical protein
SAG0530	137	OsmC/Ohr family protein
SAG0531	296	conserved hypothetical protein
SAG0532	324	conserved hypothetical protein
SAG0533	303	conserved hypothetical protein
SAG0534	465	dipeptidase
SAG0535	506	zinc ABC transporter, zinc-binding adhesion liprotein
SAG0536	86	ribosomal protein L31
SAG0537	311	DHH family protein
SAG0538	340	adenosine deaminase, putative
SAG0539	147	flavodoxin
SAG0540	91	chorismate mutase, putative
SAG0541	398	voltage-gated chloride channel family protein
SAG0542	127	IS1381, transposase OrfA
SAG0543	129	IS1381, transposase OrfB
SAG0544	115	ribosomal protein L19
SAG0545	359	prophage LambdaSa1, site-specific recombinase, phage integrase family
SAG0546	67	conserved domain protein
SAG0547	185	hypothetical protein
SAG0548	265	prophage LambdaSa1, repressor protein, putative
SAG0549	47	hypothetical protein
SAG0550	74	conserved hypothetical protein
SAG0551	52	conserved hypothetical protein
SAG0552	62	hypothetical protein
SAG0553	268	hypothetical protein
SAG0554	63	prophage LambdaSa1, transcriptional regulator, Cro/Ci family
SAG0555	249	prophage LambdaSa1, antirepressor, putative
SAG0556	47	hypothetical protein
SAG0557	76	hypothetical protein
SAG0558	74	hypothetical protein
SAG0559	286	conserved hypothetical protein
SAG0560	77	conserved hypothetical protein
SAG0561	46	hypothetical protein
SAG0562	84	hypothetical protein
SAG0563	53	hypothetical protein
SAG0564	160	conserved hypothetical protein
SAG0565	224	conserved domain protein
SAG0566	138	prophage LambdaSa1, single-strand binding protein
SAG0567	439	prophage LambdaSa1, reverse transcriptase/maturase family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0568	67	conserved hypothetical protein
SAG0569	158	conserved hypothetical protein
SAG0570	115	hypothetical protein
SAG0571	43	hypothetical protein
SAG0572	138	conserved hypothetical protein
SAG0573	54	hypothetical protein
SAG0574	89	conserved hypothetical protein
SAG0575	110	hypothetical protein
SAG0576	43	hypothetical protein
SAG0577	177	conserved hypothetical protein
SAG0578	88	conserved hypothetical protein
SAG0579	142	conserved hypothetical protein
SAG0580	111	conserved hypothetical protein, truncation
SAG0581	118	conserved hypothetical protein
SAG0582	422	conserved hypothetical protein
SAG0583	406	conserved hypothetical protein
SAG0584	62	conserved hypothetical protein, truncation
SAG0585	471	conserved hypothetical protein
SAG0586	154	conserved hypothetical protein
SAG0587	300	prophage LambdaSa1, structural protein, putative
SAG0588	71	conserved hypothetical protein
SAG0589	143	conserved hypothetical protein
SAG0590	112	conserved hypothetical protein
SAG0591	78	conserved hypothetical protein
SAG0592	111	conserved hypothetical protein
SAG0593	185	prophage LambdaSa1, structural protein
SAG0594	81	conserved hypothetical protein
SAG0595	123	conserved hypothetical protein
SAG0596	670	prophage LambdaSa1, pblA protein, internal deletion
SAG0597	506	prophage LambdaSa1, minor structural protein, putative
SAG0598	1374	prophage LambdaSa1, N-acetylmuramoyl-L-alanine amidase, family 4
SAG0599	668	prophage LambdaSa1, minor structural protein, putative
SAG0600	109	hypothetical protein
SAG0601	70	hypothetical protein
SAG0602	100	conserved hypothetical protein
SAG0603	111	conserved hypothetical protein
SAG0604	239	prophage LambdaSa1, lysin, putative
SAG0605	323	conserved hypothetical protein
SAG0606	66	conserved hypothetical protein
SAG0607	56	conserved hypothetical protein
SAG0608	59	hypothetical protein
SAG0609	NA	prophage LambdaSa1, integrase, degenerate
SAG0610	134	conserved hypothetical protein
SAG0611	NA	transposase, degenerate
SAG0612	53	conserved hypothetical protein
SAG0613	425	transmembrane protein Vexp1
SAG0614	218	ABC transporter, ATP-binding protein Vexp2

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0615	458	transmembrane protein Vexp3
SAG0616	217	DNA-binding response regulator VncR
SAG0617	439	sensor histidine kinase VncS
SAG0618	195	transposase OrfB, IS3 family, truncation
SAG0619	66	conserved hypothetical protein
SAG0620	62	hypothetical protein
SAG0621	401	rod shape-determining protein RodA, putative□
SAG0622	186	hydrolase, haloacid dehalogenase-like family
SAG0623	650	DNA gyrase, B subunit
SAG0624	574	septation ring formation regulator EzrA, putative
SAG0625	213	phosphoserine phosphatase SerB
SAG0626	161	MutT/nudix family protein
SAG0627	151	conserved hypothetical protein
SAG0628	435	enolase
SAG0629	354	conserved domain protein
SAG0630	427	3-phosphoshikimate 1-carboxyvinyltransferase
SAG0631	170	shikimate kinase
SAG0632	457	psr protein
SAG0633	451	RNA methyltransferase, TrmA family
SAG0634	70	hypothetical protein
SAG0635	245	acid phosphatase, class B
SAG0636	172	conserved hypothetical protein
SAG0637	NA	transcriptional regulator, TetR family, putative, authentic frameshift
SAG0638	109	cell wall surface anchor family protein, truncation
SAG0639	273	transposase OrfB, IS3 family
SAG0640	91	transposase OrfA, IS3 family
SAG0641	NA	Tn5252, Orf 10 protein, degenerate
SAG0642	59	hypothetical protein
SAG0643	NA	chaperonin, 33 kDa, degenerate
SAG0644	402	transcriptional regulator, AraC family
SAG0645	554	cell wall surface anchor family protein
SAG0646	307	cell wall surface anchor family protein
SAG0647	305	sortase family protein
SAG0648	260	sortase family protein
SAG0649	890	cell wall surface anchor family protein, putative
SAG0650	189	sortase family protein
SAG0651	201	protein of unknown function
SAG0652	NA	Tn5252, Orf 28 protein, degenerate
SAG0653	NA	conserved hypothetical protein, degenerate
SAG0654	34	hypothetical protein
SAG0655	57	conserved hypothetical protein
SAG0656	36	hypothetical protein
SAG0657	89	hypothetical protein
SAG0658	383	lipoprotein, putative
SAG0659	330	ABC transporter, ATP-binding protein
SAG0660	272	membrane protein
SAG0661	261	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0662	101	cylX protein
SAG0663	282	cylD protein
SAG0664	240	cylG protein
SAG0665	101	acyl carrier protein AcpC
SAG0666	158	cylZ protein
SAG0667	309	cylA protein
SAG0668	292	cylB protein
SAG0669	667	cylE protein
SAG0670	317	cylF protein
SAG0671	731	cylI protein
SAG0672	403	cylJ protein
SAG0673	191	cylK protein
SAG0674	113	hypothetical protein
SAG0675	171	putative secreted protein
SAG0676	885	proteinase, putative
SAG0677	1062	hypothetical protein
SAG0678	NA	endopeptidase O, degenerate
SAG0679	343	protein of unknown function
SAG0680	339	protein of unknown function
SAG0681	353	conserved domain protein
SAG0682	409	permease, putative
SAG0683	NA	transmembrane protein Vexp3, putative, degenerate
SAG0684	223	ABC transporter, ATP-binding protein
SAG0685	472	conserved hypothetical protein
SAG0686	261	DNA-entry nuclease, putative
SAG0687	212	DedA family protein, putative
SAG0688	218	ABC transporter, ATP-binding protein
SAG0689	257	membrane protein, putative
SAG0690	272	conserved hypothetical protein
SAG0691	294	transcriptional regulator, LysR family
SAG0692	193	regulatory protein, putative
SAG0693	377	IS1548, transposase
SAG0694	173	regulatory protein, putative, truncation
SAG0695	330	D-lactate dehydrogenase
SAG0696	516	sodium:galactoside symporter family protein, putative
SAG0697	341	2-keto-3-deoxygluconate kinase
SAG0698	599	beta-glucuronidase
SAG0699	223	transcriptional regulator, GntR family
SAG0700	205	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase
SAG0701	466	glucuronate isomerase
SAG0702	348	mannonate dehydratase
SAG0703	279	D-mannonate oxidoreductase
SAG0704	270	hydrolase, haloacid dehalogenase-like family
SAG0705	596	glycosyl hydrolase, family 3
SAG0706	361	proline dipeptidase
SAG0707	334	transcriptional regulator, RegM family
SAG0708	488	alpha amylase family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0709	332	glycosyl transferase, group 1 family protein
SAG0710	444	glycosyl transferase, group 1 family protein
SAG0711	647	threonyl-tRNA synthetase
SAG0712	234	DNA-binding response regulator
SAG0713	339	conserved hypothetical protein
SAG0714	188	conserved hypothetical protein
SAG0715	216	amino acid ABC transporter, permease protein
SAG0716	231	amino acid ABC transporter, permease protein
SAG0717	266	amino acid ABC transporter, amino acid-binding protein
SAG0718	251	amino acid ABC transporter, ATP-binding protein.
SAG0719	236	DNA-binding response regulator
SAG0720	449	sensory box histidine kinase
SAG0721	269	metallo-beta-lactamase superfamily protein
SAG0722	122	conserved hypothetical protein
SAG0723	236	ribonuclease III
SAG0724	1179	chromosome segregation SMC protein
SAG0725	265	hydrolase, haloacid dehalogenase-like family
SAG0726	274	hydrolase, haloacid dehalogenase-like family
SAG0727	536	signal recognition particle-docking protein FtsY
SAG0728	270	ABC transporter, substrate-binding protein
SAG0729	300	ABC transporter, permease protein, putative
SAG0730	42	ABC transporter, ATP-binding protein
SAG0731	347	bacterial luciferase family protein
SAG0732	720	transcriptional accessory protein Tex, putative
SAG0733	142	conserved hypothetical protein
SAG0734	87	phage shock protein C, putative
SAG0735	44	hypothetical protein
SAG0736	311	HPr(Ser) kinase/phosphatase
SAG0737	257	prolipoprotein diacylglycerol transferase
SAG0738	132	conserved hypothetical protein
SAG0739	143	conserved hypothetical protein
SAG0740	91	conserved hypothetical protein
SAG0741	303	peptidase, U32 family, putative
SAG0742	428	peptidase, U32 family
SAG0743	70	conserved hypothetical protein
SAG0744	265	membrane protein, putative
SAG0745	446	Mn ²⁺ /Fe ²⁺ transporter, NRAMP family
SAG0746	369	riboflavin biosynthesis protein RibD
SAG0747	208	riboflavin synthase, alpha subunit
SAG0748	397	riboflavin biosynthesis protein RibA
SAG0749	156	riboflavin synthase, beta subunit
SAG0750	496	lysyl-tRNA synthetase
SAG0751	300	hydrolase, haloacid dehalogenase-like family
SAG0752	213	phosphoglycerate mutase family protein
SAG0753	157	ebsC family protein, putative
SAG0754	205	conserved domain protein
SAG0755	282	peptidase, U32 family
SAG0756	174	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0757	129	protein of unknown function/lipoprotein, putative
SAG0758	599	oligoendopeptidase F, putative
SAG0759	931	phosphoenolpyruvate carboxylase
SAG0760	377	IS1548, transposase
SAG0761	422	cell division protein, FtsW/RodA/SpoVE family
SAG0762	398	translation elongation factor Tu
SAG0763	252	triosephosphate isomerase
SAG0764	230	phosphoglycerate mutase family protein
SAG0765	681	penicillin-binding protein 2b
SAG0766	198	recombination protein RecR
SAG0767	348	D-alanine--D-alanine ligase
SAG0768	455	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-- D-alanyl-D-alanyl ligase
SAG0769	406	oxalate:formate antiporter
SAG0770	228	membrane protein, putative
SAG0771	512	cell wall surface anchor family protein
SAG0772	514	peptide chain release factor 3
SAG0773	126	conserved hypothetical protein
SAG0774	244	ABC transporter, ATP-binding protein
SAG0775	220	ABC transporter, permease protein
SAG0776	276	YaeC family protein, putative
SAG0777	528	ATP-dependent RNA helicase, DEAD/DEAH box family
SAG0778	88	conserved hypothetical protein
SAG0779	254	conserved hypothetical protein
SAG0780	246	acyltransferase family protein
SAG0781	217	competence protein CeiA
SAG0782	745	DNA internalization-related competence protein ComEC/Rec2
SAG0783	269	hydrolase, haloacid dehalogenase-like family
SAG0784	314	sugar-binding transcriptional regulator, LacI family
SAG0785	330	conserved hypothetical protein
SAG0786	242	conserved domain protein
SAG0787	345	DNA polymerase III, delta subunit, putative
SAG0788	202	superoxide dismutase, Fe-Mn
SAG0789	283	transcriptional antiterminator LicT
SAG0790	622	PTS system, beta-glucosides-specific IIABC components
SAG0791	475	6-phospho-beta-glucosidase
SAG0792	364	conserved hypothetical protein
SAG0793	380	glycerate kinase 2
SAG0794	418	permease, GntP family
SAG0795	354	conserved hypothetical protein
SAG0796	147	transcriptional regulator, MarR family
SAG0797	342	S-adenosylmethionine:tRNA ribosyltransferase-isomerase
SAG0798	226	membrane protein, putative
SAG0799	233	glucosamine-6-phosphate isomerase
SAG0800	318	glutathione S-transferase family protein
SAG0801	239	ribosomal small subunit pseudouridine synthase A
SAG0802	38	hypothetical protein
SAG0803	383	major facilitator family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0804	315	competence protein CoiA
SAG0805	601	oligoendopeptidase B
SAG0806	208	hydrolase, haloacid dehalogenase-like family
SAG0807	235	O-methyltransferase family protein
SAG0808	309	protease maturation protein, putative
SAG0809	161	conserved hypothetical protein
SAG0810	872	alanyl-tRNA synthetase
SAG0811	238	membrane protein, putative
SAG0812	272	glycosyl transferase, family 8
SAG0813	81	hypothetical protein
SAG0814	95	conserved hypothetical protein
SAG0815	71	transcriptional regulator, Cro/CI family
SAG0816	253	membrane protein, putative
SAG0817	187	membrane protein, putative
SAG0818	319	ribonucleoside-diphosphate reductase 2, beta subunit
SAG0819	719	ribonucleoside-diphosphate reductase 2, alpha subunit
SAG0820	74	ribonucleoside-diphosphate reductase 2, NrdH-redoxin
SAG0821	87	phosphocarrier protein HPr
SAG0822	577	phosphoenolpyruvate-protein phosphotransferase
SAG0823	475	glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent
SAG0824	417	polysaccharide deacetylase family protein
SAG0825	360	ATP-dependent RNA helicase, DEAD/DEAH box family
SAG0826	209	uridine kinase
SAG0827	165	conserved hypothetical protein
SAG0828	554	DNA polymerase III, gamma and tau subunits
SAG0829	64	conserved hypothetical protein
SAG0830	311	biotin--acetyl-CoA-carboxylase ligase
SAG0831	398	S-adenosylmethionine synthetase
SAG0832	753	protein of unknown function
SAG0833	181	hypothetical protein
SAG0834	42	hypothetical protein
SAG0835	188	conserved hypothetical protein
SAG0836	184	conserved hypothetical protein
SAG0837	428	ABC transporter, ATP-binding protein
SAG0838	233	hypothetical protein
SAG0839	226	transcriptional regulator, TenA family
SAG0840	265	phosphomethylpyrimidine kinase
SAG0841	256	hydroxyethylthiazole kinase
SAG0842	223	thiamine-phosphate pyrophosphorylase
SAG0843	419	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
SAG0844	184	acetyltransferase, GNAT family
SAG0845	427	CBS domain protein
SAG0846	286	methionine aminopeptidase, type I
SAG0847	306	ribonuclease BN, putative
SAG0848	151	GtrA family protein
SAG0849	169	conserved hypothetical protein
SAG0850	652	DNA ligase, NAD-dependent
SAG0851	339	bmrU protein, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0852	766	pullulanase, putative
SAG0853	622	1,4-alpha-glucan branching enzyme
SAG0854	379	glucose-1-phosphate adenylyltransferase
SAG0855	NA	glycogen biosynthesis protein GlgD, authentic frameshift
SAG0856	476	glycogen synthase
SAG0857	66	ATP synthase F0, C subunit
SAG0858	238	ATP synthase F0, A subunit
SAG0859	165	ATP synthase F0, B subunit
SAG0860	178	ATP synthase F1, delta subunit
SAG0861	501	ATP synthase F1, alpha subunit
SAG0862	293	ATP synthase F1, gamma subunit
SAG0863	468	ATP synthase F1, beta subunit
SAG0864	137	ATP synthase F1, epsilon subunit
SAG0865	76	conserved hypothetical protein
SAG0866	423	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
SAG0867	63	conserved hypothetical protein
SAG0868	285	DNA-entry nuclease
SAG0869	346	phenylalanyl-tRNA synthetase, alpha subunit
SAG0870	173	acetyltransferase, GNAT family
SAG0871	801	phenylalanyl-tRNA synthetase, beta subunit
SAG0872	300	conserved hypothetical protein
SAG0873	1077	exonuclease RexB
SAG0874	1207	exonuclease RexA
SAG0875	305	magnesium transporter, CorA family, putative
SAG0876	458	tRNA modification GTPase TrmE
SAG0877	636	ABC transporter, ATP-binding protein
SAG0878	322	acetoin dehydrogenase, thymine PPi dependent, E1 component, alpha subunit
SAG0879	332	acetoin dehydrogenase, thymine PPi dependent, E1 component, beta subunit
SAG0880	462	acetoin dehydrogenase, thymine PPi dependent, E2 component, dihydrolipoamide acetyltransferase
SAG0881	585	acetoin dehydrogenase, thymine PPi dependent, E3 component, dihydrolipoamide dehydrogenase
SAG0882	329	lipoate-protein ligase A
SAG0883	261	cobyric acid synthase, putative
SAG0884	447	mur ligase family protein
SAG0885	283	conserved hypothetical protein TIGR00159
SAG0886	319	protein of unknown function
SAG0887	450	phosphoglucomutase/phosphomannomutase family protein
SAG0888	123	conserved hypothetical protein
SAG0889	126	conserved hypothetical protein
SAG0890	376	oxygen-independent coproporphyrinogen III oxidase, putative
SAG0891	245	conserved hypothetical protein
SAG0892	256	hydrolase, haloacid dehalogenase-like family
SAG0893	218	conserved hypothetical protein
SAG0894	1370	protein of unknown function
SAG0895	289	lipoyl-binding domain protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0896	108	oxidoreductase, putative
SAG0897	221	conserved hypothetical protein
SAG0898	83	hypothetical protein
SAG0899	57	hypothetical protein
SAG0900	56	hypothetical protein
SAG0901	127	hypothetical protein
SAG0902	45	hypothetical protein
SAG0903	44	hypothetical protein
SAG0904	56	hypothetical protein
SAG0905	138	nucleoside diphosphate kinase
SAG0906	610	GTP-binding protein LepA
SAG0907	877	protein of unknown function/lipoprotein, putative
SAG0908	203	HD domain protein
SAG0909	154	acetyltransferase, GNAT family
SAG0910	144	PilB-related protein
SAG0911	930	cation-transporting ATPase, E1-E2 family
SAG0912	367	nucleoside diphosphate kinase domain protein
SAG0913	212	chloramphenicol acetyltransferase
SAG0914	203	conserved hypothetical protein
SAG0915	405	Tn916, transposase
SAG0916	67	Tn916, excisionase
SAG0917	83	Tn916, hypothetical protein
SAG0918	76	Tn916, hypothetical protein
SAG0919	157	Tn916, hypothetical protein
SAG0920	23	Tn916, hypothetical protein
SAG0921	117	Tn916, transcriptional regulator, putative
SAG0922	61	Tn916, hypothetical protein
SAG0923	639	Tn916, tetracycline resistance protein
SAG0924	28	Tn916, tetM leader peptide
SAG0925	310	Tn916, hypothetical protein
SAG0926	333	Tn916, NLP/P60 family protein
SAG0927	725	membrane protein, putative
SAG0928	NA	Tn916, hypothetical protein, authentic frameshift
SAG0929	168	Tn916, hypothetical protein
SAG0930	165	Tn916, hypothetical protein
SAG0931	73	Tn916, hypothetical protein
SAG0932	401	Tn916, transcriptional regulator, putative
SAG0933	461	Tn916, FtsK/SpoIIIE family protein
SAG0934	128	Tn916, hypothetical protein
SAG0935	104	Tn916, hypothetical protein
SAG0936	39	Tn916, hypothetical protein
SAG0937	NA	ABC transporter, ATP-binding protein, authentic frameshift
SAG0938	122	transcriptional regulator, GntR family
SAG0939	1034	DNA polymerase III, alpha subunit
SAG0940	340	6-phosphofructokinase
SAG0941	500	pyruvate kinase
SAG0942	185	signal peptidase I, putative
SAG0943	47	hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0944	604	glucosamine--fructose-6-phosphate aminotransferase, isomerizing
SAG0945	377	IS1548, transposase
SAG0946	109	phnA protein
SAG0947	213	amino acid ABC transporter, permease protein
SAG0948	209	amino acid ABC transporter, ATP-binding protein
SAG0949	276	amino acid ABC transporter, amino acid-binding protein
SAG0950	82	ribosomal protein S20
SAG0951	306	pantothenate kinase
SAG0952	196	conserved hypothetical protein
SAG0953	129	cytidine deaminase
SAG0954	349	protein of unknown function/lipoprotein, putative
SAG0955	511	sugar ABC transporter, ATP-binding protein
SAG0956	353	sugar ABC transporter, permease protein, putative
SAG0957	318	sugar ABC transporter, permease protein, putative
SAG0958	456	NADH oxidase
SAG0959	329	L-lactate dehydrogenase
SAG0960	819	DNA gyrase, A subunit
SAG0961	247	sortase SrtA
SAG0962	137	glyoxylase family protein
SAG0963	320	conserved hypothetical protein
SAG0964	375	Na ⁺ /H ⁺ exchanger family protein
SAG0965	127	IS1381, transposase OrfA
SAG0966	129	IS1381, transposase OrfB
SAG0967	520	GMP synthase
SAG0968	232	transcriptional regulator, GntR family
SAG0969	444	gid protein
SAG0970	247	acetyltransferase, GNAT family
SAG0971	282	protein of unknown function/lipoprotein, putative
SAG0972	NA	conserved hypothetical protein, authentic frameshift
SAG0973	320	nisin-resistance protein, putative
SAG0974	250	ABC transporter, ATP-binding protein
SAG0975	651	ABC transporter, permease protein, putative
SAG0976	222	DNA-binding response regulator
SAG0977	312	sensor histidine kinase
SAG0978	356	site-specific recombinase, phage integrase family
SAG0979	553	ABC transporter, substrate-binding protein
SAG0980	257	conserved hypothetical protein
SAG0981	228	satD protein
SAG0982	521	signal recognition particle protein Ffh
SAG0983	110	conserved hypothetical protein
SAG0984	437	sensor histidine kinase CiaH
SAG0985	226	DNA-binding response regulator CiaR
SAG0986	849	aminopeptidase N
SAG0987	217	phosphate transport system regulatory protein PhoU
SAG0988	252	phosphate ABC transporter, ATP-binding protein PstB, putative
SAG0989	267	phosphate ABC transporter, ATP-binding protein PstB, putative
SAG0990	295	phosphate ABC transporter, permease protein PstA, putative
SAG0991	305	phosphate ABC transporter, permease protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0992	286	phosphate ABC transporter, phosphate-binding protein
SAG0993	436	NOL1/NOP2/sun family protein
SAG0994	254	inositol monophosphatase family protein
SAG0995	93	conserved hypothetical protein
SAG0996	137	conserved hypothetical protein
SAG0997	310	macrolide-efflux protein mreA/riboflavin biosynthesis protein RibF
SAG0998	294	tRNA pseudouridine synthase B
SAG0999	143	acetyltransferase, GNAT family
SAG1000	423	conserved hypothetical protein
SAG1001	196	conserved hypothetical protein
SAG1002	292	protease, putative
SAG1003	876	permease, putative
SAG1004	233	ABC transporter, ATP-binding protein
SAG1005	706	DNA topoisomerase I
SAG1006	280	DprA/SMF protein, putative DNA processing factor
SAG1007	342	iron-compound ABC transporter, iron-compound-binding protein
SAG1008	253	iron compound ABC transporter, ATP-binding protein
SAG1009	324	iron compound ABC transporter, permease protein
SAG1010	320	iron compound ABC transporter, permease protein
SAG1011	182	acetyltransferase, CysE/LacA/LpxA/NodL family
SAG1012	253	ribonuclease HII
SAG1013	283	GTP-binding protein
SAG1014	190	conserved hypothetical protein
SAG1015	494	carbon starvation protein CstA, putative
SAG1016	244	response regulator
SAG1017	579	sensor histidine kinase, putative
SAG1018	40	lipoprotein, putative
SAG1019	39	hypothetical protein
SAG1020	227	lipoprotein, putative
SAG1021	107	hypothetical protein
SAG1022	177	hypothetical protein
SAG1023	48	hypothetical protein
SAG1024	183	lipoprotein, putative
SAG1025	149	hypothetical protein
SAG1026	NA	immunogenic secreted protein, degenerate
SAG1027	84	conserved hypothetical protein
SAG1028	196	hypothetical protein
SAG1029	101	hypothetical protein
SAG1030	304	protein of unknown function
SAG1031	120	conserved domain protein
SAG1032	85	conserved hypothetical protein
SAG1033	1309	FtsK/SpoIIIE family protein
SAG1034	55	hypothetical protein
SAG1035	424	conserved hypothetical protein
SAG1036	80	conserved hypothetical protein
SAG1037	157	hypothetical protein
SAG1038	1003	phage infection protein, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1039	96	conserved hypothetical protein
SAG1040	260	conserved domain protein
SAG1041	107	hypothetical protein
SAG1042	1060	carbamoyl-phosphate synthase, large subunit
SAG1043	358	carbamoyl-phosphate synthase, small subunit
SAG1044	307	aspartate carbamoyltransferase
SAG1045	430	dihydroorotase, multifunctional complex type
SAG1046	209	orotate phosphoribosyltransferase
SAG1047	233	orotidine 5'-phosphate decarboxylase
SAG1048	410	membrane protein, putative
SAG1049	513	ABC transporter, ATP-binding protein
SAG1050	112	ribonucleotide reductase, truncation
SAG1051	358	aspartate-semialdehyde dehydrogenase
SAG1052	47	cell wall surface anchor family protein, putative
SAG1053	30	hypothetical protein
SAG1054	531	cardiolipin synthetase
SAG1055	556	formate--tetrahydrofolate ligase
SAG1056	339	lipoate-protein ligase A
SAG1057	292	conserved hypothetical protein
SAG1058	272	conserved hypothetical protein
SAG1059	110	glycine cleavage system H protein, putative
SAG1060	328	bacterial luciferase family protein
SAG1061	399	oxidoreductase, FMN-binding
SAG1062	282	lipoate-protein ligase A family protein
SAG1063	228	flavoprotein-related protein
SAG1064	180	flavoprotein family protein
SAG1065	190	membrane protein, putative
SAG1066	572	phosphoglucomutase
SAG1067	178	IS861, transposase OrfA
SAG1068	277	IS861, transposase OrfB
SAG1069	65	hypothetical protein
SAG1070	577	ABC transporter, ATP-binding/permease protein
SAG1071	573	ABC transporter, ATP-binding/permease protein
SAG1072	200	conserved hypothetical protein
SAG1073	325	conserved hypothetical protein
SAG1074	418	serine hydroxymethyltransferase
SAG1075	183	Sua5/YciO/YrdC/Ywlc family protein
SAG1076	276	modification methylase, HemK family
SAG1077	359	peptide chain release factor 1
SAG1078	189	thymidine kinases
SAG1079	60	4-oxalocrotonate tautomerase
SAG1080	47	hypothetical protein
SAG1081	312	ApbE family protein
SAG1082	200	conserved hypothetical protein
SAG1083	411	conserved hypothetical protein
SAG1084	262	formate/nitrite transporter family protein
SAG1085	424	xanthine permease
SAG1086	193	xanthine phosphoribosyltransferase

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1087	327	guanosine monophosphate reductase
SAG1088	446	drug resistance transporter, EmrB/QacA family, putative
SAG1089	230	conserved hypothetical protein
SAG1090	666	potassium uptake protein, putative
SAG1091	216	oxidoreductase, short chain dehydrogenase/reductase family
SAG1092	330	phosphate acetyltransferase
SAG1093	294	ribosomal large subunit pseudouridine synthase, RluD subfamily
SAG1094	278	conserved hypothetical protein
SAG1095	223	GTP pyrophosphokinase family protein
SAG1096	190	conserved hypothetical protein
SAG1097	324	ribose-phosphate pyrophosphokinase
SAG1098	371	cysteine desulphurase
SAG1099	115	conserved hypothetical protein
SAG1100	210	conserved hypothetical protein
SAG1101	226	DNA repair protein RadC
SAG1102	377	membrane protein, putative
SAG1103	478	6-phospho-beta-glucosidase
SAG1104	204	platelet activating factor, putative
SAG1105	273	hydrolase, haloacid dehalogenase-like family
SAG1106	309	transcriptional regulator, AraC family, putative
SAG1107	510	voltage-gated chloride channel family protein
SAG1108	357	spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein
SAG1109	258	spermidine/putrescine ABC transporter, permease protein
SAG1110	264	spermidine/putrescine ABC transporter, permease protein
SAG1111	384	spermidine/putrescine ABC transporter, ATP-binding protein
SAG1112	300	UDP-N-acetylenolpyruvoylglucosamine reductase
SAG1113	162	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
SAG1114	120	dihydroneopterin aldolase
SAG1115	267	dihydropteroate synthase
SAG1116	187	GTP cyclohydrolase I
SAG1117	420	folylpolyglutamate synthase
SAG1118	295	rarD protein
SAG1119	288	homoserine kinase
SAG1120	427	homoserine dehydrogenase
SAG1121	295	polysaccharide deacetylase family protein
SAG1122	515	transporter, BCCT family protein
SAG1123	34	hypothetical protein
SAG1124	458	aldehyde dehydrogenase family protein
SAG1125	335	membrane protein, putative
SAG1126	228	protein of unknown function
SAG1127	446	conserved domain protein
SAG1128	65	transcriptional regulator, Cro/CI family
SAG1129	36	hypothetical protein
SAG1130	49	hypothetical protein
SAG1131	164	thiol peroxidase
SAG1132	219	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1133	254	conserved hypothetical protein
SAG1134	213	transcriptional regulator, GntR family/potassium uptake protein, TrkA family
SAG1135	183	gls24 protein, putative
SAG1136	65	conserved hypothetical protein
SAG1137	180	gls24 protein, putative
SAG1138	64	conserved hypothetical protein
SAG1139	193	conserved hypothetical protein
SAG1140	82	conserved hypothetical protein
SAG1141	112	conserved hypothetical protein
SAG1142	759	ATP-dependent DNA helicase PcrA
SAG1143	128	conserved hypothetical protein
SAG1144	441	uracil permease
SAG1145	448	sodium:alanine symporter family protein
SAG1146	411	cation efflux family protein
SAG1147	130	conserved hypothetical protein
SAG1148	231	membrane protein, putative
SAG1149	207	lipoprotein, putative
SAG1150	400	ribosomal protein S1
SAG1151	76	conserved hypothetical protein
SAG1152	340	branched-chain amino acid aminotransferase
SAG1153	819	DNA topoisomerase IV, A subunit
SAG1154	653	DNA topoisomerase IV, B subunit
SAG1155	212	membrane protein, putative
SAG1156	217	uracil-DNA glycosylase
SAG1157	161	conserved hypothetical protein
SAG1158	413	CMP-N-acetylneuraminic acid synthetase NeuA
SAG1159	209	neuD protein
SAG1160	384	UDP-N-acetylglucosamine-2-epimerase NeuC
SAG1161	341	N-acetyl neuramic acid synthetase NeuB
SAG1162	466	polysaccharide biosynthesis protein CpsL
SAG1163	318	polysaccharide biosynthesis protein CpsK(V)
SAG1164	321	glycosyl transferase CpsJ(V)
SAG1165	327	glycosyl transferase CpsO(V)
SAG1166	295	glycosyl transferase CpsN(V)
SAG1167	241	polysaccharide biosynthesis protein CpsM(V)
SAG1168	364	polysaccharide biosynthesis protein cpsH(V)
SAG1169	163	glycosyl transferase CpsG(V)
SAG1170	149	polysaccharide biosynthesis protein CpsF
SAG1171	462	glycosyl transferase CpsE
SAG1172	229	cpsD protein
SAG1173	230	cpsC protein
SAG1174	243	capsular polysaccharide biosynthesis protein CpsB
SAG1175	485	capsular polysaccharide biosynthesis protein CpsA
SAG1176	290	transcriptional regulator, LysR family, putative
SAG1177	255	conserved hypothetical protein
SAG1178	236	purine nucleoside phosphorylase
SAG1179	418	voltage-gated chloride channel family protein, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1180	269	purine nucleoside phosphorylase
SAG1181	135	arsenate reductase
SAG1182	403	phosphopentomutase
SAG1183	223	ribose 5-phosphate isomerase
SAG1184	236	conserved hypothetical protein
SAG1185	262	tributylin esterase
SAG1186	553	metallo-beta-lactamase superfamily protein
SAG1187	253	ABC transporter, ATP-binding protein
SAG1188	287	ABC transporter, permease protein
SAG1189	334	conserved hypothetical protein
SAG1190	551	adherence and virulence protein A
SAG1191	239	alpha-acetolactate decarboxylase
SAG1192	560	acetolactate synthase, catabolic
SAG1193	408	TPR domain protein
SAG1194	396	membrane protein, putative
SAG1195	153	MutT/nudix family protein
SAG1196	160	mutator MutT protein
SAG1197	1072	hyaluronidase
SAG1198	348	dTDP-glucose 4,6-dehydratase
SAG1199	197	dTDP-4-dehydrorhamnose 3,5-epimerase
SAG1200	289	glucose-1-phosphate thymidyltransferase
SAG1201	367	iminodiacetate oxidase, putative
SAG1202	262	conserved hypothetical protein TIGR00486
SAG1203	227	conserved hypothetical protein
SAG1204	226	DNA replication protein DnaD, putative
SAG1205	172	adenine phosphoribosyltransferase
SAG1206	854	conserved domain protein
SAG1207	32	hypothetical protein
SAG1208	732	single-stranded-DNA-specific exonuclease RecJ
SAG1209	253	oxidoreductase, short chain dehydrogenase/reductase family
SAG1210	309	metallo-beta-lactamase superfamily protein
SAG1211	215	conserved hypothetical protein
SAG1212	412	GTP-binding protein HflX
SAG1213	296	tRNA delta(2)-isopentenylpyrophosphate transferase
SAG1214	58	hypothetical protein
SAG1215	305	exfoliative toxin A, putative
SAG1216	1252	pullulanase, putative
SAG1217	NA	conserved hypothetical protein, authentic frameshift
SAG1218	194	conserved hypothetical protein
SAG1219	468	peptidase, M20/M25/M40 family
SAG1220	200	nitroreductase family protein
SAG1221	NA	glycerophosphoryl diester phosphodiesterase, putative, authentic point mutation
SAG1222	593	excinuclease ABC, C subunit
SAG1223	255	conserved hypothetical protein
SAG1224	446	MATE efflux family protein
SAG1225	136	conserved hypothetical protein
SAG1226	165	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1227	198	protein of unknown function
SAG1228	96	ISSdy1, transposase OrfA
SAG1229	259	ISSdy1, transposase OrfB
SAG1230	96	conserved hypothetical protein
SAG1231	NA	transposase OrfB, IS3 family, degenerate
SAG1232	77	transposase OrfB, IS3 family, truncation
SAG1233	822	streptococcal histidine triad family protein
SAG1234	306	laminin-binding surface protein
SAG1235	425	GBSi1, group II intron, maturase
SAG1236	NA	C5a peptidase, authentic frameshift
SAG1237	444	hypothetical protein
SAG1238	202	hypothetical protein
SAG1239	76	conserved hypothetical protein
SAG1240	125	conserved hypothetical protein, truncation
SAG1241	91	transposase OrfA, IS3 family
SAG1242	67	transposase OrfB, IS3 family, truncation
SAG1243	96	ISSdy1, transposase OrfA
SAG1244	259	ISSdy1, transposase OrfB
SAG1245	38	hypothetical protein
SAG1246	389	hypothetical protein
SAG1247	399	site-specific recombinase, phage integrase family
SAG1248	75	conserved hypothetical protein
SAG1249	74	transcriptional regulator, Cro/CI family
SAG1250	621	Tn5252, relaxase
SAG1251	121	Tn5252, Orf 9 protein
SAG1252	120	Tn5252, Orf 10 protein
SAG1253	435	transposase, ISL3 family
SAG1254	546	mercuric reductase
SAG1255	130	mercuric resistance operon regulatory protein MerR
SAG1256	142	IS861, transposase OrfB, truncation
SAG1257	709	cation-transporting ATPase, E1-E2 family
SAG1258	122	cadmium efflux system accessory protein
SAG1259	99	conserved hypothetical protein
SAG1260	262	hypothetical protein
SAG1261	198	conserved hypothetical protein
SAG1262	695	cation-transporting ATPase, E1-E2 family
SAG1263	NA	conserved domain protein, authentic frameshift
SAG1264	148	transcriptional repressor CopY, putative
SAG1265	206	cadmium resistance transporter, putative
SAG1266	152	hypothetical protein
SAG1267	108	hypothetical protein
SAG1268	230	repressor protein, putative
SAG1269	44	hypothetical protein
SAG1270	471	ImpB/MucB/SamB family protein
SAG1271	116	conserved hypothetical protein
SAG1272	102	conserved hypothetical protein
SAG1273	118	conserved hypothetical protein
SAG1274	129	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1275	75	hypothetical protein
SAG1276	358	conserved hypothetical protein
SAG1277	163	hypothetical protein
SAG1278	96	hypothetical protein
SAG1279	99	conserved domain protein
SAG1280	2274	SNF2 family protein
SAG1281	183	hypothetical protein
SAG1282	63	calcium-binding protein, putative
SAG1283	1631	agglutinin receptor
SAG1284	196	abortive infection protein AbiGI
SAG1285	281	abortive infection protein AbiGII
SAG1286	933	Tn5252, Orf28
SAG1287	776	Tn5252, Orf26
SAG1288	NA	Tn5252, Orf25, degenerate
SAG1289	284	Tn5252, Orf23
SAG1290	80	hypothetical protein
SAG1291	605	Tn5252, Orf 21 protein, internal deletion
SAG1292	162	hypothetical protein
SAG1293	194	protease, putative
SAG1294	77	conserved hypothetical protein
SAG1295	127	conserved hypothetical protein
SAG1296	142	conserved hypothetical protein
SAG1297	451	C-5 cytosine-specific DNA methylase
SAG1298	31	hypothetical protein
SAG1299	272	conserved hypothetical protein
SAG1300	57	conserved hypothetical protein
SAG1301	121	ribosomal protein L7/L12
SAG1302	166	ribosomal protein L10
SAG1303	702	ATP-dependent Clp protease, ATP-binding subunit
SAG1304	32	hypothetical protein
SAG1305	314	homocysteine S-methyltransferase MmuM, putative
SAG1306	458	amino acid permease
SAG1307	216	hypothetical protein
SAG1308	167	hypothetical protein
SAG1309	30	hypothetical protein
SAG1310	182	transcriptional regulator, TetR family
SAG1311	198	GTP-binding protein
SAG1312	408	ATP-dependent Clp protease, ATP-binding subunit ClpX
SAG1313	56	conserved hypothetical protein
SAG1314	164	dihydrofolate reductase
SAG1315	279	thymidylate synthase
SAG1316	390	HMG-CoA synthase
SAG1317	427	3-hydroxy-3-methylglutaryl-CoA reductase
SAG1318	149	conserved hypothetical protein
SAG1319	214	hemolysin III, putative
SAG1320	304	conserved hypothetical protein TIGR00147
SAG1321	284	glutathione S-transferase family protein, putative
SAG1322	72	conserved domain protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1323	331	isopentenyl-diphosphate delta-isomerase
SAG1324	330	phosphomevalonate kinase
SAG1325	314	diphosphomevalonate decarboxylase
SAG1326	292	mevalonate kinase, putative
SAG1327	409	sensor histidine kinase
SAG1328	228	DNA-binding response regulator
SAG1329	208	GTP pyrophosphokinase family protein
SAG1330	68	hypothetical protein
SAG1331	979	R5 protein
SAG1332	146	transcriptional regulator, MarR family, putative
SAG1333	690	5'-nucleotidase family protein
SAG1334	136	polypeptide deformylase, putative
SAG1335	449	NADP-specific glutamate dehydrogenase
SAG1336	169	membrane protein, putative
SAG1337	589	ABC transporter, ATP-binding/permease protein
SAG1338	579	ABC transporter, ATP-binding/permease protein
SAG1339	157	acetyltransferase, GNAT family
SAG1340	622	ABC transporter, ATP-binding protein
SAG1341	402	polyA polymerase family protein
SAG1342	282	DegV family protein
SAG1343	126	protein of unknown function
SAG1344	177	hypothetical protein
SAG1345	164	conserved hypothetical protein
SAG1346	654	PTS system, fructose specific IIABC components
SAG1347	303	1-phosphofructokinase
SAG1348	247	lactose phosphotransferase system repressor
SAG1349	411	beta-lactam resistance factor
SAG1350	544	surface antigen-related protein
SAG1351	307	2-dehydropantoate 2-reductase, putative
SAG1352	356	regulatory protein, putative
SAG1353	330	pyridine nucleotide-disulphide oxidoreductase family protein
SAG1354	251	tRNA (guanine-N1)-methyltransferase
SAG1355	172	16S rRNA processing protein RimM
SAG1356	503	transcriptional regulator, RofA family
SAG1357	80	KH domain protein
SAG1358	90	ribosomal protein S16
SAG1359	415	permease, putative
SAG1360	236	ABC transporter, ATP-binding protein
SAG1361	414	conserved hypothetical protein
SAG1362	532	carbamoyl-phosphate synthase, large subunit, putative
SAG1363	356	carbamoyl-phosphate synthase, small subunit
SAG1364	173	pyrimidine operon regulatory protein
SAG1365	296	ribosomal large subunit pseudouridine synthase, RluD subfamily
SAG1366	154	lipoprotein signal peptidase
SAG1367	301	transcriptional regulator, LysR family
SAG1368	94	ribosomal protein L27
SAG1369	112	conserved hypothetical protein
SAG1370	104	ribosomal protein L21

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1371	392	conserved hypothetical protein
SAG1372	404	thiamine biosynthesis protein ThiI
SAG1373	381	cysteine desulphurase
SAG1374	150	conserved hypothetical protein
SAG1375	449	glutathione reductase
SAG1376	111	conserved hypothetical protein
SAG1377	388	chorismate synthase
SAG1378	355	3-dehydroquinate synthase
SAG1379	225	3-dehydroquinate dehydratase
SAG1380	385	conserved hypothetical protein
SAG1381	714	sulfatase
SAG1382	119	ribosomal protein L20
SAG1383	66	ribosomal protein L35
SAG1384	176	translation initiation factor IF-3
SAG1385	227	cytidylate kinase
SAG1386	174	conserved hypothetical protein
SAG1387	65	ferredoxin, 4Fe-4S
SAG1388	163	conserved hypothetical protein
SAG1389	406	peptidase T
SAG1390	544	polysaccharide biosynthesis protein, putative
SAG1391	484	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase
SAG1392	264	iron compound ABC transporter, ATP-binding protein
SAG1393	310	iron compound ABC transporter, substrate-binding protein
SAG1394	341	iron compound ABC transporter, permease protein
SAG1395	333	iron compound ABC transporter, permease protein
SAG1396	217	conserved hypothetical protein
SAG1397	311	inorganic pyrophosphatase, manganese-dependent
SAG1398	262	pyruvate formate-lyase-activating enzyme
SAG1399	444	CBS domain protein
SAG1400	188	conserved hypothetical protein
SAG1401	311	conserved hypothetical protein TIGR01212
SAG1402	213	PAP2 family protein
SAG1403	194	membrane protein, putative
SAG1404	308	cell wall surface anchor family protein
SAG1405	294	sortase family protein
SAG1406	293	sortase family protein
SAG1407	705	cell wall surface anchor family protein
SAG1408	901	cell wall surface anchor family protein
SAG1409	NA	rogB protein, authentic frameshift
SAG1410	379	glycosyl transferase, group 1 family protein
SAG1411	282	glycosyl transferase, group 2 family protein
SAG1412	474	polysaccharide biosynthesis protein
SAG1413	454	membrane protein, putative
SAG1414	308	glycosyl transferase, group 2 family protein
SAG1415	311	glycosyl transferase, group 2 family protein
SAG1416	352	nucleotide sugar dehydratase, putative
SAG1417	240	nucleotidyl transferase, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1418	274	polysaccharide biosynthesis protein, putative
SAG1419	577	lipoprotein, putative
SAG1420	117	conserved hypothetical protein
SAG1421	243	glycosyl transferase, group 2 family protein
SAG1422	313	glycosyl transferase, group 2 family protein
SAG1423	384	glycosyl transferase, putative
SAG1424	284	dTDP-4-dehydrorhamnose reductase
SAG1425	113	conserved hypothetical protein
SAG1426	369	RNA polymerase sigma-70 factor
SAG1427	602	DNA primase
SAG1428	125	large conductance mechanosensitive channel protein
SAG1429	58	ribosomal protein S21
SAG1430	167	conserved hypothetical protein
SAG1431	268	amino acid ABC transporter, amino acid-binding protein
SAG1432	347	ammonium transporter family protein
SAG1433	375	conserved hypothetical protein
SAG1434	328	rhodanese family protein
SAG1435	101	conserved hypothetical protein
SAG1436	457	glycerol-3-phosphate transporter, putative
SAG1437	55	hypothetical protein
SAG1438	754	glycogen phosphorylase
SAG1439	498	4-alpha-glucanotransferase
SAG1440	342	maltose operon repressor MalR, putative
SAG1441	415	maltose/maltodextrin ABC transporter, maltose/maltodextrin-binding protein
SAG1442	456	maltose ABC transporter, permease protein
SAG1443	278	maltose ABC transporter, permease protein
SAG1444	490	proton/peptide symporter family protein
SAG1445	NA	MutT/nudix family protein, authentic frameshift
SAG1446	62	hypothetical protein
SAG1447	441	conserved hypothetical protein
SAG1448	502	glycosyl transferase, group 1 family protein
SAG1449	795	preprotein translocase SecA subunit, putative
SAG1450	330	conserved domain protein
SAG1451	494	conserved hypothetical protein
SAG1452	514	conserved hypothetical protein
SAG1453	409	preprotein translocase SecY family protein
SAG1454	398	glycosyl transferase, putative
SAG1455	295	glycosyl transferase, group 2 family protein
SAG1456	NA	glycosyl transferase, family 8, degenerate
SAG1457	129	IS1381, transposase OrfB
SAG1458	127	IS1381, transposase OrfA
SAG1459	413	glycosyl transferase family 8
SAG1460	401	glycosyl transferase, family 8
SAG1461	335	conserved hypothetical protein
SAG1462	970	cell wall surface anchor family protein
SAG1463	NA	transcriptional regulator, RofA family, authentic point mutation
SAG1464	663	excinuclease ABC, B subunit

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1465	306	protease, putative
SAG1466	727	glutamine ABC transporter, glutamine-binding protein/permease protein
SAG1467	246	glutamine ABC transporter, ATP-binding protein, GlnQ putative
SAG1468	116	conserved hypothetical protein
SAG1469	52	conserved hypothetical protein
SAG1470	437	GTP-binding protein, GTP1/Obg family
SAG1471	42	conserved hypothetical protein
SAG1472	413	aminopeptidase PepS
SAG1473	192	cell wall surface anchor family protein
SAG1474	680	amidase family protein
SAG1475	240	ribosomal small subunit pseudouridine synthase A
SAG1476	280	oxidoreductase, aldo/keto reductase family
SAG1477	224	nitroreductase family protein
SAG1478	130	lactoylglutathione lyase
SAG1479	308	glycosyl transferase, group 2 family protein
SAG1480	462	amino acid permease
SAG1481	155	SsrA-binding protein
SAG1482	801	exoribonuclease, VacB/Rnb family
SAG1483	78	preprotein translocase, SecE subunit
SAG1484	48	ribosomal protein L33
SAG1485	389	multi-drug resistance protein
SAG1486	548	membrane protein, putative
SAG1487	233	ABC transporter, ATP binding protein
SAG1488	195	dephospho-CoA kinase
SAG1489	273	formamidopyrimidine-DNA glycosylase
SAG1490	282	transcriptional regulator, MutR family
SAG1491	530	hypothetical protein
SAG1492	58	hypothetical protein
SAG1493	66	hypothetical protein
SAG1494	32	hypothetical protein
SAG1495	81	CAAX amino terminal protease family protein
SAG1496	110	hypothetical protein
SAG1497	37	hypothetical protein
SAG1498	133	hypothetical protein
SAG1499	299	GTP-binding protein Era
SAG1500	132	diacylglycerol kinase
SAG1501	161	conserved hypothetical protein TIGR00043
SAG1502	268	tetracenomycin polyketide synthesis O-methyltransferase TcmP, putative
SAG1503	39	hypothetical protein
SAG1504	38	hypothetical protein
SAG1505	158	MutT/nudix family protein
SAG1506	267	hypothetical protein
SAG1507	345	PhoH family protein
SAG1508	590	67 kDa Myosin-crossreactive streptococcal antigen
SAG1509	71	conserved hypothetical protein
SAG1510	169	peptide methionine sulfoxide reductase

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1511	284	conserved hypothetical protein
SAG1512	185	ribosome recycling factor
SAG1513	242	uridylate kinase
SAG1514	226	peptide ABC transporter, ATP-binding protein
SAG1515	262	peptide ABC transporter, ATP-binding protein
SAG1516	255	peptide ABC transporter, permease protein
SAG1517	314	peptide ABC transporter, permease protein
SAG1518	538	peptide ABC transporter, peptide-binding protein
SAG1519	229	ribosomal protein L1
SAG1520	141	ribosomal protein L11
SAG1521	388	transposase, IS30 family, putative
SAG1522	460	transporter, major facilitator family
SAG1523	404	peptidase, M20/M25/M40 family
SAG1524	294	transcriptional regulator, LysR family
SAG1525	117	conserved hypothetical protein
SAG1526	178	IS861, transposase OrfA
SAG1527	277	IS861, transposase OrfB
SAG1528	571	chorismate binding enzyme
SAG1529	816	FtsK/SpoIIIE family protein
SAG1530	267	peptidyl-prolyl cis-trans isomerase, cyclophilin-type
SAG1531	277	manganese ABC transporter, permease protein
SAG1532	238	manganese ABC transporter, ATP-binding protein
SAG1533	308	manganese ABC transporter, manganese-binding adhesion liprotein
SAG1534	215	iron-dependent transcriptional regulator
SAG1535	229	5-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase
SAG1536	89	conserved hypothetical protein
SAG1537	184	MutT/nudix family protein
SAG1538	459	UDP-N-acetylglucosamine pyrophosphorylase
SAG1539	31	hypothetical protein
SAG1540	137	conserved hypothetical protein
SAG1541	125	glyoxalase family protein
SAG1542	318	oxidoreductase, Gfo/Idh/MocA family
SAG1543	NA	conserved hypothetical protein, authentic frameshift
SAG1544	232	gluconate 5-dehydrogenase, putative
SAG1545	78	conserved hypothetical protein
SAG1546	82	conserved hypothetical protein
SAG1547	166	acetyltransferase, GNAT family
SAG1548	422	glycosyl transferase, group 2 family protein
SAG1549	127	IS1381, transposase OrfA
SAG1550	129	IS1381, transposase OrfB
SAG1551	67	hypothetical protein
SAG1552	719	conserved hypothetical protein
SAG1553	477	hypothetical protein
SAG1554	225	hypothetical protein
SAG1555	231	hypothetical protein
SAG1556	445	branched-chain amino acid transport system II carrier protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1557	665	methionyl-tRNA synthetase
SAG1558	291	tellurite resistance protein TehB
SAG1559	231	membrane protein, putative
SAG1560	40	hypothetical protein
SAG1561	405	PTS system, IIC component, putative
SAG1562	280	conserved hypothetical protein
SAG1563	275	exodeoxyribonuclease
SAG1564	118	conserved hypothetical protein
SAG1565	158	methylated-DNA--protein-cysteine S-methyltransferase
SAG1566	393	D-isomer specific 2-hydroxyacid dehydrogenase family protein
SAG1567	182	acetyltransferase, GNAT family
SAG1568	NA	phosphoserine aminotransferase, authentic frameshift
SAG1569	211	copper homeostasis protein CutC, putative
SAG1570	34	conserved hypothetical protein
SAG1571	53	hypothetical protein
SAG1572	287	tetrapyrrole methylase family protein
SAG1573	108	conserved hypothetical protein
SAG1574	287	DNA polymerase III, delta prime subunit, putative
SAG1575	211	thymidylate kinase
SAG1576	267	transposase, IS30 family, putative, truncation
SAG1577	219	AcuB family protein
SAG1578	236	branched-chain amino acid ABC transporter, ATP-binding protein
SAG1579	254	branched-chain amino acid ABC transporter, ATP-binding protein
SAG1580	317	branched-chain amino acid ABC transporter, permease protein
SAG1581	289	branched-chain amino acid ABC transporter, permease protein
SAG1582	388	branched-chain amino acid ABC transporter, amino acid-binding protein
SAG1583	81	conserved hypothetical protein
SAG1584	377	IS1548, transposase
SAG1585	196	ATP-dependent Clp protease, proteolytic subunit ClpP
SAG1586	209	uracil phosphoribosyltransferase
SAG1587	389	aminotransferase, class I
SAG1588	182	RNA methyltransferase, TrmH family, group 2
SAG1589	450	amino acid permease, putative
SAG1590	449	potassium uptake protein, Trk family
SAG1591	475	cation uptake protein, Trk family
SAG1592	83	conserved hypothetical protein TIGR00278
SAG1593	240	ribosomal large subunit pseudouridine synthase B
SAG1594	194	conserved hypothetical protein TIGR00281
SAG1595	235	conserved hypothetical protein
SAG1596	246	integrase/recombinase, phage integrase family
SAG1597	157	CBS domain protein
SAG1598	173	conserved hypothetical protein
SAG1599	324	HAM1 protein
SAG1600	264	glutamate racemase
SAG1601	79	conserved hypothetical protein
SAG1602	180	membrane protein, putative
SAG1603	173	transcriptional regulator, biotin repressor family

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1604	229	membrane protein, putative
SAG1605	167	conserved hypothetical protein
SAG1606	247	RNA methyltransferase, TrmH family
SAG1607	92	acylphosphatase
SAG1608	310	lipoprotein, putative
SAG1609	221	amino acid ABC transporter, permease protein
SAG1610	285	amino acid ABC transporter, substrate-binding protein
SAG1611	486	amidase family protein
SAG1612	160	transcription elongation factor GreA
SAG1613	600	conserved hypothetical protein
SAG1614	167	acetyltransferase, GNAT family
SAG1615	443	UDP-N-acetylmuramate--alanine ligase
SAG1616	205	conserved hypothetical protein
SAG1617	32	hypothetical protein
SAG1618	1032	Snf2 family protein
SAG1619	377	IS1548, transposase
SAG1620	436	phosphoglycerate dehydrogenase-related protein
SAG1621	300	primosomal protein DnaI
SAG1622	391	conserved hypothetical protein
SAG1623	159	conserved hypothetical protein TIGR00244
SAG1624	501	sensor histidine kinase CsrS
SAG1625	229	DNA-binding response regulator CsrR
SAG1626	177	conserved hypothetical protein
SAG1627	296	heat shock protein HtpX
SAG1628	184	lemA protein
SAG1629	237	glucose-inhibited division protein B
SAG1630	459	sodium transport family protein
SAG1631	223	potassium uptake protein, Trk family, putative
SAG1632	276	cobalt transport family protein
SAG1633	558	ABC transporter, ATP-binding protein
SAG1634	212	conserved hypothetical protein
SAG1635	402	sodium:dicarboxylate symporter family protein
SAG1636	455	branched-chain amino acid transport system II carrier protein
SAG1637	351	alcohol dehydrogenase, zinc-containing
SAG1638	230	ABC transporter, permease protein
SAG1639	356	ABC transporter, ATP-binding protein
SAG1640	458	peptidase, M20/M25/M40 family
SAG1641	274	YaeC family protein
SAG1642	277	ABC transporter, substrate-binding protein
SAG1643	229	glutamine amidotransferase, class I
SAG1644	37	hypothetical protein
SAG1645	238	conserved hypothetical protein TIGR01033
SAG1646	32	hypothetical protein
SAG1647	328	dihydroxyacetone kinase family protein
SAG1648	178	transcriptional regulator, TetR family, putative
SAG1649	37	hypothetical protein
SAG1650	329	dihydroxyacetone kinase family protein
SAG1651	192	dihydroxyacetone kinase family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1652	124	conserved hypothetical protein
SAG1653	237	glycerol uptake facilitator protein
SAG1654	134	conserved hypothetical protein
SAG1655	237	transcriptional regulator, MerR family
SAG1656	369	conserved hypothetical protein
SAG1657	83	hypothetical protein
SAG1658	244	conserved hypothetical protein
SAG1659	118	iojap-related protein
SAG1660	173	isochorismatase family protein
SAG1661	195	conserved hypothetical protein TIGR00488
SAG1662	210	conserved hypothetical protein TIGR00482
SAG1663	105	conserved hypothetical protein TIGR00253
SAG1664	372	GTP-binding protein
SAG1665	177	hydrolase, haloacid dehalogenase-like family
SAG1666	304	membrane protein, putative
SAG1667	480	glutamyl-tRNA(Gln) amidotransferase, B subunit
SAG1668	488	glutamyl-tRNA(Gln) amidotransferase, A subunit
SAG1669	100	glutamyl-tRNA(Gln) amidotransferase, C subunit
SAG1670	881	pyruvate phosphate dikinase
SAG1671	276	protein of unknown function
SAG1672	170	CBS domain protein
SAG1673	321	3-hydroxyacyl-CoA dehydrogenase family protein
SAG1674	182	isochorismatase family protein
SAG1675	261	transcriptional regulator CodY, putative
SAG1676	403	aminotransferase, class I
SAG1677	150	conserved hypothetical protein
SAG1678	460	hydrolase, haloacid dehalogenase-like family
SAG1679	320	asparaginase family protein
SAG1680	292	shikimate 5-dehydrogenase
SAG1681	304	oxidoreductase, aldo/keto reductase family
SAG1682	671	ATP-dependent DNA helicase RecG
SAG1683	512	immunogenic secreted protein, putative
SAG1684	366	alanine racemase
SAG1685	119	holo-(acyl-carrier-protein) synthase
SAG1686	335	phospho-2-dehydro-3-deoxyheptonate aldolase
SAG1687	842	preprotein translocase, SecA subunit
SAG1688	315	mannose-6-phosphate isomerase, class I
SAG1689	293	fructokinase
SAG1690	639	PTS system, IIABC components
SAG1691	479	sucrose-6-phosphate hydrolase
SAG1692	320	sucrose operon repressor ScrR
SAG1693	144	N utilization substance protein B
SAG1694	129	conserved hypothetical protein
SAG1695	186	translation elongation factor P
SAG1696	38	hypothetical protein
SAG1697	48	hypothetical protein
SAG1698	99	conserved hypothetical protein
SAG1699	30	hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1700	76	hypothetical protein
SAG1701	56	hypothetical protein
SAG1702	41	hypothetical protein
SAG1703	54	hypothetical protein
SAG1704	150	cytidine/deoxycytidylate deaminase family protein
SAG1705	NA	peptidase, M24 family, authentic point mutation
SAG1706	238	conserved hypothetical protein
SAG1707	499	drug resistance transporter, EmrB/QacA family
SAG1708	38	hypothetical protein
SAG1709	942	excinuclease ABC, A subunit
SAG1710	223	conserved hypothetical protein
SAG1711	314	magnesium transporter, CorA family
SAG1712	79	ribosomal protein S18
SAG1713	163	single-strand binding protein
SAG1714	95	ribosomal protein S6
SAG1715	374	A/G-specific adenine glycosylase
SAG1716	197	transcriptional regulator, Cro/CI family
SAG1717	104	thioredoxin
SAG1718	166	PAP2 family protein
SAG1719	779	MutS2 family protein
SAG1720	180	conserved hypothetical protein
SAG1721	103	conserved hypothetical protein
SAG1722	297	ribonuclease HIII
SAG1723	197	signal peptidase I
SAG1724	806	helicase, putative
SAG1725	160	conserved hypothetical protein
SAG1726	364	DNA-damage-inducible protein P
SAG1727	770	formate acetyltransferase
SAG1728	124	FMN-binding protein
SAG1729	309	conserved hypothetical protein
SAG1730	251	conserved hypothetical protein
SAG1731	298	membrane protein, putative
SAG1732	282	glycerol uptake facilitator protein, putative
SAG1733	150	universal stress protein family
SAG1734	400	transporter, putative
SAG1735	219	transcriptional regulator, Crp/Fnr family
SAG1736	761	X-pro dipeptidyl-peptidase
SAG1737	119	hypothetical protein
SAG1738	326	polyprenyl synthetase family protein
SAG1739	582	ABC transporter, ATP-binding protein CydC
SAG1740	572	ABC transporter, ATP-binding protein CydD
SAG1741	339	cytochrome d ubiquinol oxidase, subunit II
SAG1742	475	cytochrome d oxidase, subunit I
SAG1743	402	pyridine nucleotide-disulphide oxidoreductase family protein
SAG1744	299	prenyltransferase, UbiA family
SAG1745	148	hypothetical protein
SAG1746	35	hypothetical protein
SAG1747	99	conserved hypothetical protein TIGR00103

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1748	396	cyclopropane-fatty-acyl-phospholipid synthase
SAG1749	241	transcriptional regulator, merR family
SAG1750	195	exonuclease
SAG1751	178	conserved hypothetical protein
SAG1752	390	conserved hypothetical protein TIGR00275
SAG1753	260	conserved hypothetical protein
SAG1754	89	ribosomal protein S14
SAG1755	38	hypothetical protein
SAG1756	341	conserved hypothetical protein
SAG1757	336	O-sialoglycoprotein endopeptidase family protein
SAG1758	135	ribosomal-protein-alanine acetyltransferase, putative
SAG1759	230	protein of unknown function
SAG1760	76	conserved hypothetical protein
SAG1761	559	metallo-beta-lactamase superfamily protein
SAG1762	169	conserved hypothetical protein
SAG1763	448	glutamine synthetase, type I
SAG1764	123	transcriptional regulator GlnR
SAG1765	179	conserved hypothetical protein
SAG1766	398	phosphoglycerate kinase
SAG1767	289	acid phosphatase
SAG1768	336	glyceraldehyde 3-phosphate dehydrogenase
SAG1769	692	translation elongation factor G
SAG1770	156	ribosomal protein S7
SAG1771	137	ribosomal protein S12
SAG1772	270	pur operon repressor
SAG1773	313	HD domain protein
SAG1774	424	conserved hypothetical protein
SAG1775	210	conserved hypothetical protein
SAG1776	220	ribulose-phosphate 3-epimerase
SAG1777	290	conserved hypothetical protein TIGR00157
SAG1778	283	rRNA (guanine-N1-)-methyltransferase, putative
SAG1779	290	dimethyladenosine transferase
SAG1780	163	hypothetical protein
SAG1781	186	primase-related protein
SAG1782	260	deoxyribonuclease, TatD family
SAG1783	90	hypothetical protein
SAG1784	130	hypothetical protein
SAG1785	430	hypothetical protein
SAG1786	130	protein of unknown function
SAG1787	420	dltD protein
SAG1788	79	D-alanyl carrier protein
SAG1789	421	dltB protein
SAG1790	511	D-alanine-activating enzyme
SAG1791	395	sensor histidine kinase
SAG1792	224	DNA-binding response regulator
SAG1793	44	ribosomal protein L34
SAG1794	451	membrane protein, putative
SAG1795	388	transposase, IS30 family, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1796	575	amino acid ABC transporter, permease protein
SAG1797	407	amino acid ABC transporter, ATP-binding protein
SAG1798	39	hypothetical protein
SAG1799	792	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase
SAG1800	363	conserved hypothetical protein
SAG1801	559	transcriptional antiterminator, BglG family
SAG1802	253	conserved hypothetical protein
SAG1803	505	carbohydrate kinase, FGGY family
SAG1804	329	hypothetical protein
SAG1805	483	PTS system, IIC component, putative
SAG1806	318	glyoxylate reductase, NADH-dependent
SAG1807	339	hypothetical protein
SAG1808	327	sugar binding transcriptional regulator, LacI family
SAG1809	215	transaldolase family protein
SAG1810	238	carbohydrate isomerase, AraD/FucA family
SAG1811	287	hexulose-6-phosphate isomerase, putative
SAG1812	221	hexulose-6-phosphate synthase, putative
SAG1813	161	PTS system, IIA component
SAG1814	92	PTS system, IIB component
SAG1815	479	transport protein SgaT, putative
SAG1816	205	hypothetical protein
SAG1817	157	hypothetical protein
SAG1818	430	adenylosuccinate synthetase
SAG1819	340	perfringolysin O regulator protein
SAG1820	224	conserved hypothetical protein
SAG1821	750	glutamate--cysteine ligase/amino acid ligase, putative
SAG1822	272	protein of unknown function
SAG1823	418	protein of unknown function
SAG1824	291	chaperonin, 33 kDa
SAG1825	325	NifR3/Smm1 family protein
SAG1826	213	deoxynucleoside kinase family protein
SAG1827	163	phosphinothricin N-acetyltransferase
SAG1828	815	ATP-dependent Clp protease, ATP-binding subunit
SAG1829	154	transcriptional regulator CtsR
SAG1830	153	conserved hypothetical protein
SAG1831	346	translation elongation factor Ts
SAG1832	256	ribosomal protein S2
SAG1833	186	alkyl hydroperoxide reductase, subunit C
SAG1834	510	alkyl hydroperoxide reductase, subunit F
SAG1835	134	conserved hypothetical protein
SAG1836	61	conserved hypothetical protein
SAG1837	468	prophage LambdaSa2, lysin, putative
SAG1838	109	prophage LambdaSa2, holin, putative
SAG1839	136	conserved hypothetical protein
SAG1840	112	hypothetical protein
SAG1841	76	conserved domain protein
SAG1842	1224	prophage LambdaSa2, PblB, putative
SAG1843	240	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1844	911	conserved hypothetical protein
SAG1845	42	hypothetical protein
SAG1846	158	hypothetical protein
SAG1847	227	conserved hypothetical protein
SAG1848	114	conserved hypothetical protein
SAG1849	115	hypothetical protein
SAG1850	101	hypothetical protein
SAG1851	111	conserved domain protein
SAG1852	420	conserved domain protein
SAG1853	180	prophage LambdaSa2, protease, putative
SAG1854	380	conserved hypothetical protein
SAG1855	570	prophage LambdaSa2, terminase large subunit, putative
SAG1856	161	hypothetical protein
SAG1857	119	prophage LambdaSa2, HNH endonuclease family protein
SAG1858	95	hypothetical protein
SAG1859	180	prophage LambdaSa2, site-specific recombinase, phage integrase family
SAG1860	154	conserved hypothetical protein
SAG1861	119	prophage LambdaSa2, transcriptional regulator, Cro/CI family
SAG1862	86	hypothetical protein
SAG1863	138	prophage LambdaSa2, single-strand binding protein
SAG1864	68	hypothetical protein
SAG1865	74	conserved hypothetical protein
SAG1866	109	conserved hypothetical protein
SAG1867	163	conserved hypothetical protein
SAG1868	134	hypothetical protein
SAG1869	437	prophage LambdaSa2, type II DNA modification methyltransferase, putative
SAG1870	273	prophage LambdaSa2, DNA replication protein DnaC, putative
SAG1871	248	prophage LambdaSa2, bacteriophage replication protein/hypothetical protein, truncation/fusion
SAG1872	200	hypothetical protein
SAG1873	443	prophage LambdaSa2, replicative DNA helicase
SAG1874	87	hypothetical protein
SAG1875	94	conserved hypothetical protein
SAG1876	176	prophage LambdaSa2, HNH endonuclease family protein
SAG1877	236	prophage LambdaSa2, antirepressor protein, putative
SAG1878	102	conserved domain protein
SAG1879	156	hypothetical protein
SAG1880	54	hypothetical protein
SAG1881	51	hypothetical protein
SAG1882	120	prophage LambdaSa2, repressor protein, putative
SAG1883	128	conserved hypothetical protein
SAG1884	134	hypothetical protein
SAG1885	356	prophage LambdaSa2, site-specific recombinase, phage integrase family
SAG1886	32	hypothetical protein
SAG1887	689	Na ⁺ /H ⁺ exchanger family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1888	78	hypothetical protein
SAG1889	317	microcin immunity protein MccF, putative
SAG1890	631	endopeptidase O
SAG1891	327	oxidoreductase, Gfo/Idh/MocA family
SAG1892	358	membrane protein, putative
SAG1893	59	hypothetical protein
SAG1894	214	cyclic nucleotide-binding domain protein
SAG1895	204	polypeptide deformylase
SAG1896	333	sugar binding transcriptional regulator RegR
SAG1897	634	conserved hypothetical protein
SAG1898	271	PTS system, IID component
SAG1899	288	PTS system, IIC component
SAG1900	164	PTS system, IIB component
SAG1901	398	glucuronyl hydrolase
SAG1902	144	PTS system, IIA component
SAG1903	34	hypothetical protein
SAG1904	270	oxidoreductase, short-chain dehydrogenase/reductase family
SAG1905	212	conserved hypothetical protein
SAG1906	335	carbohydrate kinase, PfkB family
SAG1907	212	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase
SAG1908	499	hypothetical protein
SAG1909	204	nitroreductase family protein
SAG1910	141	transcriptional regulator, MarR family
SAG1911	1468	DNA polymerase III, alpha subunit, Gram-positive type
SAG1912	194	N-acetylmuramoyl-L-alanine amidase, family 4 protein
SAG1913	617	prolyl-tRNA synthetase
SAG1914	419	membrane-associated zinc metalloprotease, putative
SAG1915	264	phosphatidate cytidyltransferase
SAG1916	250	undecaprenyl diphosphate synthase
SAG1917	113	preprotein translocase, YajC subunit
SAG1918	114	bacteriocin transport accessory protein, putative
SAG1919	387	malate oxidoreductase
SAG1920	445	citrate carrier protein, CCS family
SAG1921	508	sensor histidine kinase
SAG1922	229	response regulator
SAG1923	331	UDP-glucose 4-epimerase
SAG1924	535	glucan 1,6-alpha-glucosidase
SAG1925	377	sugar ABC transporter, ATP-binding protein
SAG1926	283	helix-turn-helix domain protein, fis-type
SAG1927	298	lacX protein
SAG1928	325	tagatose 1,6-diphosphate aldolase
SAG1929	310	tagatose-6-phosphate kinase
SAG1930	171	galactose-6-phosphate isomerase, LacB subunit
SAG1931	141	galactose-6-phosphate isomerase, LacA subunit
SAG1932	816	neuraminidase-related protein
SAG1933	482	PTS system, IIC component, putative
SAG1934	101	PTS system, IIB component, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1935	157	PTS system, IIA component, putative
SAG1936	258	lactose phosphotransferase system repressor
SAG1937	NA	streptococcal histidine triad family protein, degenerate
SAG1938	307	adhesion lipoprotein
SAG1939	147	protein of unknown function TIGR00256
SAG1940	738	GTP pyrophosphokinase family protein
SAG1941	800	2',3'-cyclic-nucleotide 2'-phosphodiesterase
SAG1942	151	nrdI protein
SAG1943	345	conserved hypothetical protein
SAG1944	165	conserved hypothetical protein
SAG1945	345	iron ABC transporter, iron-binding protein
SAG1946	257	DNA-binding response regulator
SAG1947	549	conserved hypothetical protein
SAG1948	275	PTS system, IID component
SAG1949	269	PTS system, IIC component
SAG1950	163	PTS system, IIB component
SAG1951	141	PTS system, IIA component, putative
SAG1952	353	membrane protein, putative
SAG1953	60	hypothetical protein
SAG1954	384	membrane protein, putative
SAG1955	282	ABC transporter, ATP-binding protein
SAG1956	96	conserved hypothetical protein, truncation
SAG1957	250	response regulator
SAG1958	276	conserved hypothetical protein
SAG1959	727	PTS system, IIABC components
SAG1960	551	sensor histidine kinase
SAG1961	225	phosphate regulon response regulator PhoB
SAG1962	218	phosphate transport system regulatory protein PhoU, putative
SAG1963	253	phosphate ABC transporter, ATP-binding protein
SAG1964	292	phosphate ABC transporter, permease protein
SAG1965	281	phosphate ABC transporter, permease protein
SAG1966	293	hemolysin precursor, putative
SAG1967	195	hypothetical protein
SAG1968	246	conserved hypothetical protein TIGR00046
SAG1969	317	ribosomal protein L11 methyltransferase
SAG1970	102	conserved hypothetical protein
SAG1971	41	hypothetical protein
SAG1972	238	transcriptional regulator, MerR family
SAG1973	156	acetyltransferase, GNAT family
SAG1974	152	MutT/nudix family protein
SAG1975	47	hypothetical protein
SAG1976	156	conserved hypothetical protein
SAG1977	163	acetyltransferase, GNAT family
SAG1978	422	ATPase, AAA family
SAG1979	253	membrane protein, putative
SAG1980	300	ABC transporter, ATP-binding protein
SAG1981	68	hypothetical protein
SAG1982	359	transcriptional regulator, Cro/CI family

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1983	105	conserved hypothetical protein
SAG1984	188	conserved hypothetical protein TIGR00730
SAG1985	51	hypothetical protein
SAG1986	375	site-specific recombinase, phage integrase family
SAG1987	61	conserved hypothetical protein
SAG1988	342	conserved hypothetical protein
SAG1989	139	hypothetical protein
SAG1990	127	hypothetical protein
SAG1991	204	transcriptional regulator, Cro/CI family
SAG1992	518	protein of unknown function
SAG1993	373	site-specific recombinase, phage integrase family
SAG1994	108	conserved hypothetical protein
SAG1995	210	hypothetical protein
SAG1996	263	cell wall surface anchor family protein, putative
SAG1997	182	hypothetical protein
SAG1998	457	hypothetical protein
SAG1999	47	hypothetical protein
SAG2000	666	membrane protein, putative
SAG2001	756	conjugal transfer protein, interruption-C
SAG2002	129	IS1381, transposase OrfB
SAG2003	127	IS1381, transposase OrfA
SAG2004	67	conjugal transfer protein, interruption-N
SAG2005	136	conserved hypothetical protein
SAG2006	88	conserved hypothetical protein
SAG2007	317	conserved hypothetical protein
SAG2008	84	conserved hypothetical protein
SAG2009	88	conserved hypothetical protein
SAG2010	157	hypothetical protein
SAG2011	160	conserved hypothetical protein
SAG2012	90	hypothetical protein
SAG2013	189	hypothetical protein
SAG2014	449	hypothetical protein
SAG2015	99	transcriptional regulator, Cro/CI family
SAG2016	125	hypothetical protein
SAG2017	429	transcriptional regulator, Cro/CI family
SAG2018	553	FtsK/SpoIIIE family protein
SAG2019	153	hypothetical protein
SAG2020	98	hypothetical protein
SAG2021	826	cell wall surface anchor family protein
SAG2022	417	transposase, ISL3 family
SAG2023	546	mercuric reductase
SAG2024	130	mercuric resistance operon regulatory protein MerR
SAG2025	522	Mn ²⁺ /Fe ²⁺ transporter, NRAMP family
SAG2026	240	membrane protein, putative
SAG2027	205	ABC transporter, ATP-binding protein
SAG2028	36	conserved hypothetical protein
SAG2029	284	streptomycin resistance protein
SAG2030	130	hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG2031	202	hypothetical protein
SAG2032	111	conserved hypothetical protein
SAG2033	162	acetyltransferase, GNAT family
SAG2034	247	membrane protein, putative
SAG2035	300	ABC transporter, ATP-binding protein
SAG2036	68	hypothetical protein
SAG2037	358	transcriptional regulator, Cro/CI family
SAG2038	204	PAP2 family protein
SAG2039	98	conserved hypothetical protein
SAG2040	186	conserved hypothetical protein TIGR00730
SAG2041	287	protease, putative
SAG2042	100	rhodanese family protein
SAG2043	255	cAMP factor
SAG2044	62	hypothetical protein
SAG2045	179	DNA topology modulation protein FlaR, putative
SAG2046	361	glycerol dehydrogenase, putative
SAG2047	235	conserved hypothetical protein
SAG2048	614	5-methyltetrahydrofolate--homocysteine methyltransferase, putative
SAG2049	745	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
SAG2050	107	conserved hypothetical protein
SAG2051	230	branched-chain amino acid transport protein AzlC, putative
SAG2052	41	hypothetical protein
SAG2053	1570	serine protease, subtilase family, putative
SAG2054	228	DNA-binding response regulator
SAG2055	462	sensor histidine kinase
SAG2056	202	chromosome assembly-related protein
SAG2057	833	leucyl-tRNA synthetase
SAG2058	415	major facilitator family protein
SAG2059	281	protein of unknown function
SAG2060	398	glycosyl transferase, family 8
SAG2061	401	glycosyl transferase, family 8
SAG2062	179	transcription antitermination protein NusG
SAG2063	630	pathogenicity protein, putative
SAG2064	57	preprotein translocase, SecE subunit, putative
SAG2065	50	ribosomal protein L33
SAG2066	773	penicillin-binding protein 2A
SAG2067	294	ribosomal large subunit pseudouridine synthase, RluD subfamily
SAG2068	546	conserved hypothetical protein
SAG2069	403	phosphopentomutase
SAG2070	223	deoxyribose-phosphate aldolase
SAG2071	400	Na ⁺ dependent nucleoside transporter
SAG2072	259	uridine phosphorylase
SAG2073	245	transcriptional regulator, GntR family
SAG2074	540	60 kda chaperonin
SAG2075	94	chaperonin, 10 kDa
SAG2076	267	ABC transporter, ATP-binding protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG2077	298	ABC transporter, permease protein
SAG2078	320	protein of unknown function/lipoprotein, putative
SAG2079	265	hydrolase, haloacid dehalogenase-like family
SAG2080	286	glyoxalase family protein
SAG2081	243	conserved hypothetical protein
SAG2082	205	anaerobic ribonucleoside-triphosphate reductase activating protein
SAG2083	163	acetyltransferase, GNAT family
SAG2084	310	virulence factor MviM, putative
SAG2085	47	conserved hypothetical protein
SAG2086	723	anaerobic ribonucleoside-triphosphate reductase
SAG2087	495	membrane protein, putative
SAG2088	40	hypothetical protein
SAG2089	105	conserved hypothetical protein
SAG2090	136	conserved hypothetical protein TIGR00250
SAG2091	88	conserved hypothetical protein
SAG2092	132	conserved hypothetical protein
SAG2093	379	recA protein
SAG2094	NA	competence/damage-inducible protein CinA, authentic frameshift
SAG2095	183	DNA-3-methyladenine glycosylase I
SAG2096	196	Holliday junction DNA helicase RuvA
SAG2097	418	transporter, putative
SAG2098	659	DNA mismatch repair protein HexB
SAG2099	33	hypothetical protein
SAG2100	67	cold shock protein, CSD family
SAG2101	858	DNA mismatch repair protein HexA
SAG2102	145	arginine repressor ArgR, putative
SAG2103	563	arginyl-tRNA synthetase
SAG2104	102	conserved hypothetical protein
SAG2105	290	conserved hypothetical protein
SAG2106	314	conserved hypothetical protein
SAG2107	583	aspartyl-tRNA synthetase
SAG2108	426	histidyl-tRNA synthetase
SAG2109	60	ribosomal protein L32
SAG2110	49	ribosomal protein L33
SAG2111	173	conserved hypothetical protein
SAG2112	494	site-specific recombinase, phage integrase family
SAG2113	82	conserved hypothetical protein
SAG2114	342	conserved hypothetical protein
SAG2115	143	hypothetical protein
SAG2116	151	conserved hypothetical protein
SAG2117	71	hypothetical protein
SAG2118	306	transcriptional regulator, Cro/CI family
SAG2119	373	conserved domain protein
SAG2120	269	hypothetical protein
SAG2121	223	hypothetical protein
SAG2122	223	DNA-binding response regulator
SAG2123	454	sensor histidine kinase
SAG2124	517	membrane protein, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG2125	308	carbamate kinase
SAG2126	332	ornithine carbamoyltransferase
SAG2127	431	sensor histidine kinase
SAG2128	277	response regulator
SAG2129	240	amino acid ABC transporter, ATP-binding protein
SAG2130	504	amino acid ABC transporter, amino acid-binding protein/permease protein
SAG2131	847	membrane protein, putative
SAG2132	247	conserved hypothetical protein
SAG2133	118	conserved hypothetical protein
SAG2134	772	membrane protein, putative
SAG2135	179	transcriptional regulator, TetR family, putative
SAG2136	98	conserved hypothetical protein
SAG2137	203	ribosomal protein S4
SAG2138	95	conserved hypothetical protein
SAG2139	451	replicative DNA helicase
SAG2140	150	ribosomal protein L9
SAG2141	660	DHH family protein
SAG2142	613	glucose inhibited division protein A
SAG2143	203	membrane protein, putative
SAG2144	373	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
SAG2145	222	L-serine dehydratase, iron-sulfur-dependent, beta subunit
SAG2146	290	L-serine dehydratase, iron-sulfur-dependent, alpha subunit
SAG2147	234	protein of unknown function/lipoprotein, putative
SAG2148	179	LysM domain protein
SAG2149	264	cobalt transport family protein
SAG2150	280	ABC transporter, ATP-binding protein
SAG2151	279	ABC transporter, ATP-binding protein
SAG2152	180	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
SAG2153	427	peptidase, M16 family
SAG2154	414	conserved hypothetical protein
SAG2155	117	conserved hypothetical protein
SAG2156	369	recF protein
SAG2157	278	transporter, putative
SAG2158	220	transcriptional regulator, Cro/CI family
SAG2159	493	inosine-5'-monophosphate dehydrogenase
SAG2160	161	transcriptional regulator, ArgR family
SAG2161	226	transcriptional regulator, Crp/Fnr family
SAG2162	234	conserved hypothetical protein
SAG2163	410	arginine deiminase
SAG2164	136	acetyltransferase, GNAT family
SAG2165	337	ornithine carbamoyltransferase
SAG2166	475	arginine/ornithine antiporter
SAG2167	318	carbamate kinase
SAG2168	341	tryptophanyl-tRNA synthetase
SAG2169	230	membrane protein, putative
SAG2170	290	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG2171	539	ABC transporter, ATP-binding protein
SAG2172	859	ABC transporter, permease protein, putative
SAG2173	159	conserved hypothetical protein TIGR00246
SAG2174	409	serine protease
SAG2175	257	partitioning protein, ParB family

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo- protein	Other	Western blot	FACS	GBS specific	Annotation
SAG0017	447	+							pcsB
SAG0031	299	+							peptidase, M23/M37 family
SAG0032	434	+				+	+		group B streptococcal surface immunogenic protein
SAG0034	438	+		+		+	+		sugar ABC transporter, sugar-binding protein
SAG0051	126	+				+	+		MORN motif family protein
SAG0079	212				+	+	+		adenylate kinase
SAG0086	85			+				+	lipoprotein, putative
SAG0093	250	+				+	+		D-alanyl-D-alanine carboxypeptidase family protein
SAG0094	191	+							N-acetylmuramoyl-L-alanine amidase, family 4 protein
SAG0108	308	+							conserved hypothetical protein
SAG0114	322	+		+					ribose ABC transporter, periplasmic D-ribose-binding protein
SAG0124	356	+							sensor histidine kinase
SAG0132	294	+				+	+		SPFH domain/Band 7 family protein
SAG0134	96	+						+	hypothetical protein
SAG0146	395	+							penicillin-binding protein 4, putative
SAG0147	411	+							D-alanyl-D-alanine carboxypeptidase family protein
SAG0148	551			+		+	-		oligopeptide ABC transporter, substrate-binding protein, putative
SAG0166	123	+							conserved domain protein
SAG0176	94	+							conserved hypothetical protein
SAG0187	542	+		+		+	+		oligopeptide ABC transporter, oligopeptide-binding protein
SAG0206	60			+				+	lipoprotein, putative
SAG0213	39	+						+	hypothetical protein
SAG0231	135	+							hypothetical protein
SAG0242	308			+		+	-		amino acid ABC transporter, amino acid-binding protein
SAG0245	152			+		+	-	+	protein of unknown function/lipoprotein, putative
SAG0255	315	+							conserved hypothetical protein
SAG0257	53			+				+	lipoprotein, putative
SAG0265	235	+				+	-	+	conserved hypothetical protein
SAG0290	270	+				+	+		ABC transporter, substrate-binding protein
SAG0298	750	+							penicillin-binding protein 1A

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo- protein	Other	Western blot	FACS	GBS specific	Annotation
SAG0306	535	+							KH domain protein
SAG0321	339	+							sensor histidine kinase, putative
SAG0329	106	+							PTS system, cellobiose-specific IIB component
SAG0368	435	+				+	+		protein of unknown function
SAG0371	167	+						+	hypothetical protein
SAG0383	334	+		+		+	-		protein of unknown function/lipoprotein, putative
SAG0392	521	+	+			+	+		cell wall surface anchor family protein
SAG0394	345				+				sensor histidine kinase
SAG0405	347	+		+		+	+		protein of unknown function/lipoprotein, putative
SAG0406	299	+							UTP-glucose-1-phosphate uridylyltransferase
SAG0407	338	+							glycerol-3-phosphate dehydrogenase (NAD(P)+)
SAG0416	1233	+	+			+	+		protease, putative
SAG0421	1055		+			+	-		cell wall surface anchor family protein
SAG0433	1389		+						surface protein Rib
SAG0437	123			+					lipoprotein, putative
SAG0451	149	+		+				+	bacteriocin transport accessory protein, putative
SAG0455	357	+							conserved hypothetical protein
SAG0472	126	+				+	-		rhodanese-like family protein
SAG0482	84	+							YGGT family protein
SAG0499	275				+				hemolysin A
SAG0503	279	+				+	+		lipase/acylhydrolase
SAG0504	200	+							conserved hypothetical protein
SAG0506	65	+						+	hypothetical protein
SAG0521	236	+							carboxymethylenebutenolidase-related protein
SAG0535	506	+				+	+		zinc ABC transporter, zinc-binding adhesion liprotein
SAG0596	670				+				prophage LambdaSa1, pblA protein, internal deletion
SAG0603	111				+				conserved hypothetical protein
SAG0604	239				+				prophage LambdaSa1, lysin, putative
SAG0617	439				+				sensor histidine kinase VncS
SAG0624	574	+							septation ring formation regulator EzrA, putative
SAG0629	354	+							conserved domain protein
SAG0635	245	+				+	-		acid phosphatase, class B
SAG0638	109	+							cell wall surface anchor family protein, interruption-N

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo- protein	Other	Western blot	FACS	GBS specific	Annotation
SAG0645	554		+			+	+		cell wall surface anchor family protein
SAG0646	307	+	+			+	-		cell wall surface anchor family protein
SAG0647	305	+							sortase family protein
SAG0649	890		+			+	+		cell wall surface anchor family protein, putative
SAG0658	383	+		+					lipoprotein, putative
SAG0675	171	+							putative secreted protein
SAG0676	885				+				proteinase, putative
SAG0677	1062		+						hypothetical protein
SAG0679	343	+		+		+	-		protein of unknown function
SAG0680	339	+				+	-		protein of unknown function
SAG0681	353	+							conserved domain protein
SAG0686	261	+				+	+		DNA-entry nuclease, putative
SAG0714	188	+						+	conserved hypothetical protein
SAG0717	266	+				+	+		amino acid ABC transporter, amino acid-binding protein
SAG0720	449				+				sensory box histidine kinase
SAG0738	132	+							conserved hypothetical protein
SAG0739	143	+							conserved hypothetical protein
SAG0742	428				+	+	+		peptidase, U32 family
SAG0755	282	+							peptidase, U32 family
SAG0757	129	+		+		+	-		protein of unknown function/lipoprotein, putative
SAG0764	230				+	+	+		phosphoglycerate mutase family protein
SAG0765	681	+							penicillin-binding protein 2b
SAG0771	512	+	+			+	+	+	cell wall surface anchor family protein
SAG0776	276	+		+					YaeC family protein, putative
SAG0777	528				+	+	+		ATP-dependent RNA helicase, DEAD/DEAH box family
SAG0785	330	+							conserved hypothetical protein
SAG0808	309	+		+		+	+		protease maturation protein, putative
SAG0824	417	+							polysaccharide deacetylase family protein
SAG0832	753	+				+	+		protein of unknown function
SAG0833	181	+						+	hypothetical protein
SAG0867	63	+							conserved hypothetical protein
SAG0868	285	+				+	-		DNA-entry nuclease
SAG0886	319	+				+	+		protein of unknown function

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo- protein	Other	Western blot	FACS	GBS specific	Annotation
SAG0904	56	+						+	hypothetical protein
SAG0907	877	+		+		+	-		protein of unknown function/lipoprotein, putative
SAG0926	333	+							Tn916, NLP/P60 family protein
SAG0942	185	+				+	+		signal peptidase I, putative
SAG0949	276	+		+		+	+		amino acid ABC transporter, amino acid-binding protein
SAG0954	349			+		+	-		protein of unknown function/lipoprotein, putative
SAG0961	247	+				+	-		sortase SrtA
SAG0963	320	+							conserved hypothetical protein
SAG0971	282	+		+		+	-		protein of unknown function/lipoprotein, putative
SAG0973	320	+						+	nisin-resistance protein, putative
SAG0977	312				+				sensor histidine kinase
SAG0979	553	+		+		+	-		ABC transporter, substrate-binding protein
SAG0984	437	+							sensor histidine kinase CiaH
SAG0992	286	+		+		+	+		phosphate ABC transporter, phosphate-binding protein
SAG1007	342	+		+		+	-		iron-compound ABC transporter, iron-compound-binding protein
SAG1014	190	+				-	-		conserved hypothetical protein
SAG1018	40			+				+	lipoprotein, putative
SAG1024	183	+		+					lipoprotein, putative
SAG1029	101	+							hypothetical protein
SAG1030	304	+				+	+		protein of unknown function
SAG1037	157	+						+	hypothetical protein
SAG1052	47		+					+	cell wall surface anchor family protein, putative
SAG1072	200	+							conserved hypothetical protein
SAG1094	278				+	+	+		conserved hypothetical protein
SAG1108	357	+				+	-		spermidine/putrescine ABC transporter, spermidine/putrescine-binding prot.
SAG1121	295	+							polysaccharide deacetylase family protein
SAG1126	228	+				+	+		protein of unknown function
SAG1127	446	+						+	conserved domain protein
SAG1130	49	+						+	hypothetical protein
SAG1138	64	+							conserved hypothetical protein
SAG1139	193	+							conserved hypothetical protein

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo- protein	Other	Western blot	FACS	GBS specific	Annotation
SAG1149	207	+		+					lipoprotein, putative
SAG1184	236	+							conserved hypothetical protein
SAG1186	553				+				metallo-beta-lactamase superfamily protein
SAG1189	334	+							conserved hypothetical protein
SAG1190	551				+				adherence and virulence protein A
SAG1197	1072	+							hyaluronidase
SAG1201	367	+							iminodiacetate oxidase, putative
SAG1206	854	+							conserved domain protein
SAG1214	58	+							hypothetical protein
SAG1216	1252		+			+	-		pullulanase, putative
SAG1227	198	+				+	-		protein of unknown function
SAG1233	822	+				+	-		streptococcal histidine triad family protein
SAG1234	306	+		+		+	+		laminin-binding surface protein
SAG1238	202	+							hypothetical protein
SAG1283	1631		+			+	+		agglutinin receptor
SAG1313	56	+							conserved hypothetical protein
SAG1327	409	+							sensor histidine kinase
SAG1331	979	+	+			+	+		R5 protein
SAG1333	690	+	+			+	+		5'-nucleotidase family protein
SAG1350	544	+							surface antigen-related protein
SAG1361	414	+							conserved hypothetical protein
SAG1371	392	+							conserved hypothetical protein
SAG1393	310			+					iron compound ABC transporter, substrate-binding protein
SAG1404	308	+	+			+	-		cell wall surface anchor family protein
SAG1405	294	+			+	+	+		sortase family protein
SAG1406	293	+							sortase family protein
SAG1407	705	+	+			+	+		cell wall surface anchor family protein
SAG1408	901		+						cell wall surface anchor family protein
SAG1419	577			+				+	lipoprotein, putative
SAG1431	268			+					amino acid ABC transporter, amino acid-binding protein
SAG1433	375	+							conserved hypothetical protein
SAG1441	415	+				+	+		maltose/maltodextrin ABC transporter, maltose/maltodextrin-binding protein

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo- protein	Other	Western blot	FACS	GBS specific	Annotation
SAG1462	970		+						cell wall surface anchor family protein
SAG1473	192	+	+					+	cell wall surface anchor family protein
SAG1474	680	+	+						amidase family protein
SAG1483	78	+							preprotein translocase, SecE subunit
SAG1488	195	+				+	+		dephospho-CoA kinase
SAG1491	530	+						+	hypothetical protein
SAG1508	590				+	+	-		67 kDa Myosin-crossreactive streptococcal antigen
SAG1518	538	+		+					peptide ABC transporter, peptide-binding protein
SAG1530	267	+		+		+	-		peptidyl-prolyl cis-trans isomerase, cyclophilin-type
SAG1533	308	+		+		+	-		manganese ABC transporter, manganese-binding adhesion liprotein
SAG1544	232	+							gluconate 5-dehydrogenase, putative
SAG1551	67	+						+	hypothetical protein
SAG1552	719	+							conserved hypothetical protein
SAG1553	477	+						+	hypothetical protein
SAG1562	280	+							conserved hypothetical protein
SAG1582	388	+		+		+	-		branched-chain amino acid ABC transporter, amino acid- binding protein
SAG1590	449				+	+	+		potassium uptake protein, Trk family
SAG1601	79	+							conserved hypothetical protein
SAG1610	285			+		+	-		amino acid ABC transporter, substrate-binding protein
SAG1618	1032				+	+	+		Snf2 family protein
SAG1624	501	+							sensor histidine kinase CsrS
SAG1628	184	+							lemA protein
SAG1631	223	+				+	-		potassium uptake protein, Trk family, putative
SAG1641	274	+				+	-		YaeC family protein
SAG1642	277	+		+		+	-		ABC transporter, substrate-binding protein
SAG1683	512	+							immunogenic secreted protein, putative
SAG1706	238	+							conserved hypothetical protein
SAG1745	148	+						+	hypothetical protein
SAG1752	390	+							conserved hypothetical protein TIGR00275
SAG1759	230				+	+	+		protein of unknown function
SAG1762	169	+							conserved hypothetical protein

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo- protein	Other	Western blot	FACS	GBS specific	Annotation
SAG1767	289	+		+					acid phosphatase
SAG1768	336				+	+	+		glyceraldehyde 3-phosphate dehydrogenase
SAG1774	424	+							conserved hypothetical protein
SAG1786	130	+				+	-		protein of unknown function
SAG1787	420	+							dltD protein
SAG1791	395	+							sensor histidine kinase
SAG1822	272	+				+	-		protein of unknown function
SAG1823	418				+	+	+		protein of unknown function
SAG1837	468				+				prophage LambdaSa2, lysin, putative
SAG1838	109	+							prophage LambdaSa2, holin, putative
SAG1839	136	+							conserved hypothetical protein
SAG1842	1224				+				prophage LambdaSa2, PblB, putative
SAG1912	194	+							N-acetylmuramoyl-L-alanine amidase, family 4 protein
SAG1921	508	+							sensor histidine kinase
SAG1932	816	+							neuraminidase-related protein
SAG1938	307	+		+		+	-		adhesion lipoprotein
SAG1941	800	+	+			+	-		2',3'-cyclic-nucleotide 2'-phosphodiesterase
SAG1945	345	+							iron ABC transporter, iron-binding protein
SAG1947	549				+				conserved hypothetical protein
SAG1960	551				+	+	+		sensor histidine kinase
SAG1966	293			+		+	-		hemolysin precursor, putative
SAG1996	263	+	+						cell wall surface anchor family protein, putative
SAG1997	182	+							hypothetical protein
SAG1998	457	+							hypothetical protein
SAG2021	826		+						cell wall surface anchor family protein
SAG2043	255	+							cAMP factor
SAG2053	1570	+	+						serine protease, subtilase family, putative
SAG2055	462				+				sensor histidine kinase
SAG2056	202	+						+	chromosome assembly-related protein
SAG2063	630	+	+						pathogenicity protein, putative
SAG2078	320	+		+		+	-		protein of unknown function/lipoprotein, putative
SAG2094		+				+	+		competence/damage-inducible protein CinA, authentic frameshift

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo- protein	Other	Western blot	FACS	GBS specific	Annotation
SAG2121	223	+						+	hypothetical protein
SAG2123	454	+							sensor histidine kinase
SAG2141	660	+				+	-		DHH family protein
SAG2147	234	+		+		+	+		protein of unknown function/lipoprotein, putative
SAG2148	179	+							LysM domain protein
SAG2174	409	+							serine protease
SAG0013	428	+				+	-		protein of unknown function

Table 3

ORF	Annotation
SAG0038	conserved hypothetical protein
SAG0048	transcriptional regulator Cro/CI family
SAG0091	transcriptional regulator ComX1 putative
SAG0137	conserved hypothetical protein
SAG0686	DNA-entry nuclease putative
SAG0770	membrane protein putative
SAG0868	DNA-entry nuclease
SAG1143	conserved hypothetical protein
SAG1233	streptococcal histidine triad family protein
SAG1596	integrase/recombinase phage integrase family
SAG1616	conserved hypothetical protein
SAG1721	conserved hypothetical protein.

Table 4: Probable recently duplicated genes

Probable recently duplicated genes are indicated on the same line and are separated by a semicolon.

SAG0148 oligopeptide ABC transporter, substrate-binding protein, putative; SAG0979 ABC transporter, substrate-binding protein

SAG0151 oligopeptide ABC transporter, ATP-binding protein; SAG1515 peptide ABC transporter, ATP-binding protein

SAG0195 IS1548, transposase; SAG0693 IS1548, transposase; SAG0760 IS1548, transposase; SAG0945 IS1548, transposase; SAG1584 IS1548, transposase; SAG1619 IS1548, transposase

SAG0230 conserved hypothetical protein; SAG1039 conserved hypothetical protein

SAG0233 hypothetical protein; SAG1785 hypothetical protein

SAG0261 IS1381, transposase OrfB; SAG0542 IS1381, transposase OrfA; SAG0543 IS1381, transposase OrfB; SAG0966 IS1381, transposase OrfB; SAG1457 IS1381, transposase OrfB; SAG1550 IS1381, transposase OrfB; SAG2002 IS1381, transposase OrfB

SAG0262 IS1381, transposase OrfA; SAG0965 IS1381, transposase OrfA; SAG1549 IS1381, transposase OrfA; SAG1458 IS1381, transposase OrfA; SAG2003 IS1381, transposase OrfA

SAG0383 protein of unknown function/lipoprotein, putative; SAG0785 conserved hypothetical protein

SAG0405 protein of unknown function/lipoprotein, putative; SAG0954 protein of unknown function/lipoprotein, putative

SAG0417 glycosyl transferase, group 2 family protein; SAG1422 glycosyl transferase, group 2 family protein

SAG0429 oxidoreductase, aldo/keto reductase family; SAG1476 oxidoreductase, aldo/keto reductase family

Table 4: Probable recently duplicated genes

SAG0432	transcriptional regulator, AraC family; SAG0644 transcriptional regulator, AraC family
SAG0434	transposase, IS256 family, truncation; SAG0448 transposase, IS256 family
SAG0438	bacteriophage L54a, integrase, truncation; SAG1986 site-specific recombinase, phage integrase family; SAG1989 hypothetical protein; SAG1993 site-specific recombinase, phage integrase family; SAG2115 hypothetical protein
SAG0442	acetyltransferase, GNAT family; SAG0443 acetyltransferase, GNAT family
SAG0447	magnesium transporter, CorA family; SAG0875 magnesium transporter, CorA family, putative
SAG0508	beta-lactam resistance factor; SAG1349 beta-lactam resistance factor
SAG0566	prophage LambdaSa1, single-strand binding protein; SAG1713 single-strand binding protein; SAG1863 prophage LambdaSa2, single-strand binding protein
SAG0603	conserved hypothetical protein; SAG1838 prophage LambdaSa2, holin, putative
SAG0604	prophage LambdaSa1, lysin, putative; SAG1837 prophage LambdaSa2, lysin, putative
SAG0618	transposase OrfB, IS3 family, truncation; SAG0639 transposase OrfB, IS3 family; SAG1232 transposase OrfB, IS3 family, truncation; SAG1242 transposase OrfB, IS3 family, truncation
SAG0640	transposase OrfA, IS3 family; SAG1241 transposase OrfA, IS3 family
SAG0646	cell wall surface anchor family protein; SAG1404 cell wall surface anchor family protein

Table 4: Probable recently duplicated genes

SAG0647 sortase family protein; SAG0648 sortase family protein; SAG0650 sortase family protein

SAG0649 cell wall surface anchor family protein, putative; SAG1408 cell wall surface anchor family protein

SAG0676 proteinase, putative; SAG2053 serine protease, subtilase family, putative

SAG0679 protein of unknown function; SAG0680 protein of unknown function; SAG0681 conserved domain protein

SAG1002 protease, putative; SAG1465 protease, putative

SAG1025 hypothetical protein; SAG1033 FtsK/SpoIIIE family protein

SAG1067 IS861, transposase OrfA; SAG1526 IS861, transposase OrfA

SAG1068 IS861, transposase OrfB; SAG1256 IS861, transposase OrfB, truncation; SAG1527 IS861, transposase OrfB

SAG1140 conserved hypothetical protein; SAG1141 conserved hypothetical protein

SAG1164 glycosyl transferase CpsI(V); SAG1165 glycosyl transferase CpsO(V)

SAG1182 phosphopentomutase; SAG2069 phosphopentomutase

SAG1225 conserved hypothetical protein; SAG1540 conserved hypothetical protein

SAG1228 ISSdy1, transposase OrfA; SAG1243 ISSdy1, transposase OrfA

SAG1229 ISSdy1, transposase OrfB; SAG1244 ISSdy1, transposase OrfB

SAG1253 transposase, ISL3 family; SAG2022 transposase, ISL3 family

Table 4: Probable recently duplicated genes

SAG1254 mercuric reductase; SAG2023 mercuric reductase
SAG1255 mercuric resistance operon regulatory protein MerR; SAG2024 mercuric resistance operon regulatory protein MerR
SAG1259 conserved hypothetical protein; SAG1272 conserved hypothetical protein
SAG1283 agglutinin receptor; SAG2021 cell wall surface anchor family protein
SAG1297 C-5 cytosine-specific DNA methylase; SAG1869 prophage LambdaSa2, type II DNA modification methyltransferase, putative
SAG1405 sortase family protein; SAG1406 sortase family protein
SAG1414 glycosyl transferase, group 2 family protein; SAG1415 glycosyl transferase, group 2 family protein
SAG1456 glycosyl transferase, family 8, degenerate; SAG2060 glycosyl transferase, family 8
SAG1521 transposase, IS30 family, putative; SAG1576 transposase, IS30 family, putative, truncation; SAG1795 transposase, IS30 family, putative
SAG1655 transcriptional regulator, MerR family; SAG1972 transcriptional regulator, MerR family
SAG1979 membrane protein, putative; SAG2034 membrane protein, putative
SAG1980 ABC transporter, ATP-binding protein; SAG2035 ABC transporter, ATP-binding protein
SAG1982 transcriptional regulator, Cro/CI family; SAG2037 transcriptional regulator, Cro/CI family
SAG1983 conserved hypothetical protein; SAG2039 conserved hypothetical protein

Table 4: Probable recently duplicated genes

SAG1984 conserved hypothetical protein TIGR00730; SAG2040 conserved hypothetical protein TIGR00730
SAG1988 conserved hypothetical protein; SAG2114 conserved hypothetical protein

Table 5

Strain	Source	Capsular serotype	Reference
090	Lancefield	Ia	
515	Houston	Ia	(1)
A909	Lancefield	Ia	(2)
Davis	Channing	Ia	
DK1	Houston	Ia	
DK8	Houston	Ia	
H36b	Lancefield	Ib	(2)
(S7) 7357b	Channing	Ib	(3)
18RS21	Lancefield	II	(4)
DK21	Houston	II	
COH1	Seattle	III	(5)
COH31	Seattle	III	(6)
D136C	Lancefield	III	(4)
M781	Houston	III	(7)
M732	Houston	III	(8)
1169NT1	Atlanta	V	(9)
2603V/R	Italy	V	This study
CJB111	Houston	V	(10)
JM9130013	Japan	VIII	(11)
SMU014	Japan	VIII	(11)
CJB110	Houston	Nontypeable	(12)

Table 5

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Table 6**Cluster 1**

SAG0230	conserved hypothetical protein
SAG0231	hypothetical protein
SAG0232	hypothetical protein
SAG0233	hypothetical protein
SAG0234	hypothetical protein
SAG0235	hypothetical protein

Cluster 2

SAG0222	conserved domain protein
SAG0223	conserved hypothetical protein, fusion
SAG0225	hypothetical protein
SAG0226	recombination protein
SAG0227	hypothetical protein
SAG0228	conserved hypothetical protein
SAG0229	conserved hypothetical protein

Cluster 3

SAG0634	hypothetical protein
SAG0635	acid phosphatase, class B
SAG0636	conserved hypothetical protein
SAG0638	cell wall surface anchor family protein, interruption-N
SAG0640	transposase OrfA, IS3 family

Table 6

SAG0642	hypothetical protein
SAG0643	chaperonin, 33 kDa, degenerate
SAG0644	transcriptional regulator, AraC family
SAG0645	cell wall surface anchor family protein
SAG0646	cell wall surface anchor family protein
SAG0647	sortase family protein
SAG0648	sortase family protein
SAG0649	cell wall surface anchor family protein, putative
SAG0650	sortase family protein
SAG0651	protein of unknown function

Cluster 4

SAG1898	PTS system, IID component
SAG1899	PTS system, IIC component
SAG1900	PTS system, IIB component
SAG1901	glucuronyl hydrolase
SAG1902	PTS system, IIA component
SAG1905	conserved hypothetical protein
SAG1906	carbohydrate kinase, PfkB family

Cluster 5

SAG0247	hypothetical protein
SAG0248	hypothetical protein

Table 6

SAG0249	hypothetical protein
SAG0674	hypothetical protein
SAG0675	putative secreted protein
SAG0676	proteinase, putative
SAG0677	hypothetical protein
SAG0680	protein of unknown function
SAG0681	conserved domain protein
SAG0684	ABC transporter, ATP-binding protein
SAG1698	conserved hypothetical protein

Cluster 6

SAG0261	IS1381, transposase OrfB
SAG0262	IS1381, transposase OrfA
SAG0965	IS1381, transposase OrfA
SAG0966	IS1381, transposase OrfB
SAG2002	IS1381, transposase OrfB

Cluster 7

SAG1027	conserved hypothetical protein
SAG1028	hypothetical protein
SAG1029	hypothetical protein
SAG1030	protein of unknown function
SAG1031	conserved domain protein

Table 6

SAG1032 conserved hypothetical protein

Cluster 8

SAG1253 transposase, ISL3 family

SAG1254 mercuric reductase

SAG1255 mercuric resistance operon regulatory protein MerR

SAG2022 transposase, ISL3 family

SAG2023 mercuric reductase

SAG2024 mercuric resistance operon regulatory protein MerR

Cluster 9

SAG1993 site-specific recombinase, phage integrase family

SAG1994 conserved hypothetical protein

SAG1995 hypothetical protein

SAG1996 cell wall surface anchor family protein, putative

SAG1997 hypothetical protein

SAG1998 hypothetical protein

SAG2000 membrane protein, putative

SAG2001 conjugal transfer protein, interruption-C

SAG2007 conserved hypothetical protein

SAG2008 conserved hypothetical protein

SAG2009 conserved hypothetical protein

SAG2010 hypothetical protein

Table 6

SAG2011	conserved hypothetical protein
SAG2012	hypothetical protein
SAG2016	hypothetical protein
SAG2017	transcriptional regulator, Cro/CI family
SAG2025	Mn ²⁺ /Fe ²⁺ transporter, NRAMP family

Cluster 10

SAG1039	conserved hypothetical protein
SAG1447	conserved hypothetical protein
SAG1448	glycosyl transferase, group 1 family protein
SAG1449	preprotein translocase SecA subunit, putative
SAG1450	conserved domain protein
SAG1452	conserved hypothetical protein
SAG1453	preprotein translocase SecY family protein
SAG1454	glycosyl transferase, putative
SAG1455	glycosyl transferase, group 2 family protein
SAG1456	glycosyl transferase, family 8, degenerate
SAG1459	glycosyl transferase family 8
SAG1460	glycosyl transferase, family 8
SAG1461	conserved hypothetical protein
SAG1462	cell wall surface anchor family protein
SAG1463	transcriptional regulator, RofA family, authentic point mutation
SAG1469	conserved hypothetical protein

Table 6

SAG1471	conserved hypothetical protein
SAG1933	PTS system, IIC component, putative

Cluster 11

SAG0009	hypothetical protein
SAG0120	hypothetical protein
SAG0157	deoxyribonuclease-related protein, degenerate
SAG0186	hypothetical protein
SAG0216	hypothetical protein
SAG0236	hypothetical protein
SAG0307	hypothetical protein
SAG0308	ABC transporter, ATP-binding protein
SAG0311	DNA-binding response regulator, authentic point mutation
SAG0518	peptide chain release factor 2, programmed frameshift
SAG0553	hypothetical protein
SAG0555	prophage LambdaSa1, antirepressor, putative
SAG0564	conserved hypothetical protein
SAG0579	conserved hypothetical protein
SAG0580	conserved hypothetical protein, truncation
SAG0611	transposase, degenerate
SAG0637	transcriptional regulator, TetR family, putative, authentic frameshift
SAG0641	Tn5252, Orf 10 protein, degenerate
SAG0652	Tn5252, Orf 28 protein, degenerate

Table 6

SAG0655	conserved hypothetical protein
SAG0678	endopeptidase O, degenerate
SAG0683	transmembrane protein Vexp3, putative, degenerate
SAG0855	glycogen biosynthesis protein GlgD, authentic frameshift
SAG0898	hypothetical protein
SAG0899	hypothetical protein
SAG0901	hypothetical protein
SAG0902	hypothetical protein
SAG0903	hypothetical protein
SAG0917	Tn916, hypothetical protein
SAG0920	Tn916, hypothetical protein
SAG0922	Tn916, hypothetical protein
SAG0924	Tn916, tetM leader peptide
SAG0928	Tn916, hypothetical protein, authentic frameshift
SAG0936	Tn916, hypothetical protein
SAG0943	hypothetical protein
SAG0972	conserved hypothetical protein, authentic frameshift
SAG1023	hypothetical protein
SAG1080	hypothetical protein
SAG1123	hypothetical protein
SAG1129	hypothetical protein
SAG1136	conserved hypothetical protein
SAG1217	conserved hypothetical protein, authentic frameshift

Table 6

SAG1231	transposase OrfB, IS3 family, degenerate
SAG1242	transposase OrfB, IS3 family, truncation
SAG1309	hypothetical protein
SAG1331	R5 protein
SAG1437	hypothetical protein
SAG1445	MutT/nudix family protein, authentic frameshift
SAG1484	ribosomal protein L33
SAG1493	hypothetical protein
SAG1539	hypothetical protein
SAG1543	conserved hypothetical protein, authentic frameshift
SAG1560	hypothetical protein
SAG1568	phosphoserine aminotransferase, authentic frameshift
SAG1570	conserved hypothetical protein
SAG1601	conserved hypothetical protein
SAG1644	hypothetical protein
SAG1646	hypothetical protein
SAG1699	hypothetical protein
SAG1705	peptidase, M24 family, authentic point mutation
SAG1708	hypothetical protein
SAG1857	prophage LambdaSa2, HNH endonuclease family protein
SAG1864	hypothetical protein
SAG1868	hypothetical protein

Table 6

SAG1869	prophage LambdaSa2, type II DNA modification methyltransferase, putative
SAG1872	hypothetical protein
SAG1874	hypothetical protein
SAG1876	prophage LambdaSa2, HNH endonuclease family protein
SAG1878	conserved domain protein
SAG1881	hypothetical protein
SAG1883	conserved hypothetical protein
SAG1886	hypothetical protein
SAG1903	hypothetical protein
SAG1937	streptococcal histidine triad family protein, degenerate
SAG1971	hypothetical protein
SAG1979	membrane protein, putative
SAG1980	ABC transporter, ATP-binding protein
SAG1981	hypothetical protein
SAG1982	transcriptional regulator, Cro/CI family
SAG1983	conserved hypothetical protein
SAG1984	conserved hypothetical protein TIGR00730
SAG1985	hypothetical protein
SAG1991	transcriptional regulator, Cro/CI family
SAG1992	protein of unknown function
SAG1999	hypothetical protein
SAG2004	conjugal transfer protein, interruption-N

Table 6

SAG2039	conserved hypothetical protein
SAG2044	hypothetical protein
SAG2052	hypothetical protein
SAG2065	ribosomal protein L33
SAG2094	competence/damage-inducible protein CinA, authentic frameshift
SAG2099	hypothetical protein

Cluster 12

SAG1164	glycosyl transferase CpsJ(V)
SAG1165	glycosyl transferase CpsO(V)
SAG1166	glycosyl transferase CpsN(V)
SAG1167	polysaccharide biosynthesis protein CpsM(V)
SAG1168	polysaccharide biosynthesis protein cpsH(V)

Cluster 13

SAG0581	conserved hypothetical protein
SAG0582	conserved hypothetical protein
SAG0583	conserved hypothetical protein
SAG0585	conserved hypothetical protein
SAG0586	conserved hypothetical protein
SAG0587	prophage LambdaSa1, structural protein, putative
SAG0588	conserved hypothetical protein
SAG0589	conserved hypothetical protein

Table 6

SAG0590	conserved hypothetical protein
SAG0591	conserved hypothetical protein
SAG0593	prophage LambdaSa1, structural protein
SAG0594	conserved hypothetical protein
SAG0595	conserved hypothetical protein
SAG0596	prophage LambdaSa1, pblA protein, internal deletion

Cluster 14

SAG0915	Tn916, transposase
SAG0918	Tn916, hypothetical protein
SAG0919	Tn916, hypothetical protein
SAG0921	Tn916, transcriptional regulator, putative
SAG0925	Tn916, hypothetical protein
SAG0926	Tn916, NLP/P60 family protein
SAG0927	membrane protein, putative
SAG0929	Tn916, hypothetical protein
SAG0930	Tn916, hypothetical protein
SAG0931	Tn916, hypothetical protein
SAG0932	Tn916, transcriptional regulator, putative
SAG0933	Tn916, FtsK/SpoIIIE family protein
SAG0934	Tn916, hypothetical protein
SAG0935	Tn916, hypothetical protein
SAG0937	ABC transporter, ATP-binding protein, authentic frameshift

Table 6**Cluster 15**

SAG1835	conserved hypothetical protein
SAG1837	prophage LambdaSa2, lysin, putative
SAG1839	conserved hypothetical protein
SAG1840	hypothetical protein
SAG1842	prophage LambdaSa2, PblB, putative
SAG1843	conserved hypothetical protein
SAG1844	conserved hypothetical protein
SAG1849	hypothetical protein
SAG1851	conserved domain protein
SAG1852	conserved domain protein
SAG1853	prophage LambdaSa2, protease, putative
SAG1854	conserved hypothetical protein
SAG1855	prophage LambdaSa2, terminase large subunit, putative
SAG1856	hypothetical protein
SAG1858	hypothetical protein
SAG1859	prophage LambdaSa2, site-specific recombinase, phage integrase family
SAG1860	conserved hypothetical protein
SAG1861	prophage LambdaSa2, transcriptional regulator, Cro/CI family
SAG1862	hypothetical protein
SAG1863	prophage LambdaSa2, single-strand binding protein
SAG1865	conserved hypothetical protein

Table 6

SAG1866	conserved hypothetical protein
SAG1867	conserved hypothetical protein
SAG1870	prophage LambdaSa2, DNA replication protein DnaC, putative
SAG1871	prophage LambdaSa2, bacteriophage replication protein/hypothetical protein, truncation/fusion
SAG1873	prophage LambdaSa2, replicative DNA helicase
SAG1877	prophage LambdaSa2, antirepressor protein, putative
SAG1879	hypothetical protein
SAG1882	prophage LambdaSa2, repressor protein, putative
SAG1884	hypothetical protein
SAG1885	prophage LambdaSa2, site-specific recombinase, phage integrase family

Cluster 16

SAG1247	site-specific recombinase, phage integrase family
SAG1250	Tn5252, relaxase
SAG1251	Tn5252, Orf 9 protein
SAG1252	Tn5252, Orf 10 protein
SAG1256	IS861, transposase OrfB, truncation
SAG1257	cation-transporting ATPase, E1-E2 family
SAG1258	cadmium efflux system accessory protein
SAG1259	conserved hypothetical protein
SAG1260	hypothetical protein
SAG1261	conserved hypothetical protein

Table 6

SAG1262	cation-transporting ATPase, E1-E2 family
SAG1263	conserved domain protein, authentic frameshift
SAG1264	transcriptional repressor CopY, putative
SAG1265	cadmium resistance transporter, putative
SAG1266	hypothetical protein
SAG1267	hypothetical protein
SAG1268	repressor protein, putative
SAG1270	ImpB/MucB/SamB family protein
SAG1271	conserved hypothetical protein
SAG1272	conserved hypothetical protein
SAG1273	conserved hypothetical protein
SAG1274	conserved hypothetical protein
SAG1276	conserved hypothetical protein
SAG1277	hypothetical protein
SAG1278	hypothetical protein
SAG1279	conserved domain protein
SAG1280	SNF2 family protein
SAG1281	hypothetical protein
SAG1283	agglutinin receptor
SAG1284	abortive infection protein AbiGI
SAG1285	abortive infection protein AbiGII
SAG1286	Tn5252, Orf28
SAG1287	Tn5252, Orf26

Table 6

SAG1288	Tn5252, Orf25, degenerate
SAG1289	Tn5252, Orf23
SAG1290	hypothetical protein
SAG1291	Tn5252, Orf 21 protein, internal deletion
SAG1292	hypothetical protein
SAG1293	protease, putative
SAG1294	conserved hypothetical protein
SAG1295	conserved hypothetical protein
SAG1296	conserved hypothetical protein
SAG1297	C-5 cytosine-specific DNA methylase
SAG1299	conserved hypothetical protein
SAG1304	hypothetical protein

Table 7

Locus	Annotation
Housekeeping	
SAG0466	thiolase
SAG0471	glucokinase
SAG0492	amino acid ABC transporter, ATP-binding protein
SAG0767	D-alanine--D-alanine ligase
SAG1086	xanthine phosphoribosyltransferase
SAG1600	glutamate racemase
SAG1680	shikimate 5-dehydrogenase
SAG1723	signal peptidase I
Surface-exposed	
SAG0079	adenylate kinase
SAG0093	D-alanyl-D-alanine carboxypeptidase family protein
SAG0163	competence protein CglA
SAG0290	ABC transporter, substrate-binding protein
SAG0368	protein of unknown function
SAG0503	lipase/acylhydrolase
SAG1473	cell wall surface anchor family protein
SAG1552	conserved hypothetical protein
SAG1641	YaeC family protein
SAG2147	protein of unknown function/lipoprotein, putative
SAG2148	LysM domain protein

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF00003 PcsB protein (pscB)
ORF00004 ribose-phosphate pyrophosphokinase (prsA)
ORF00005 aminotransferase, class I
ORF00006 recombination protein O
ORF00009 fatty acid/phospholipid synthesis protein PlsX (plsX)
ORF00011 phosphoribosylaminoimidazole-succinocarboxamide synthase (purC)
ORF00012 phosphoribosylformylglycinamide synthase, putative
ORF00013 amidophosphoribosyltransferase (purF)
ORF00014 phosphoribosylformylglycinamide cyclo-ligase (purM)
ORF00015 phosphoribosylglycinamide formyltransferase (purN)
ORF00020 group B streptococcal surface immunogenic protein
ORF00021 N-acetylmannosamine-6-P epimerase, putative
ORF00022 sugar ABC transporter, sugar-binding protein
ORF00023 sugar ABC transporter, permease protein
ORF00024 sugar ABC transporter, permease protein
ORF00026 conserved hypothetical protein
ORF00027 N-acetylneuraminate lyase, putative
ORF00028 expressed ROK family protein
ORF00030 phosphosugar-binding transcriptional regulator, RpiR family, putative
ORF00031 phosphoribosylamine--glycine ligase (purD)
ORF00032 phosphoribosylaminoimidazole carboxylase, catalytic subunit (purE)
ORF00033 phosphoribosylaminoimidazole carboxylase, ATPase subunit (purK)
ORF00036 adenylosuccinate lyase (purB)
ORF00037 transcriptional regulator, Cro/C1 family
ORF00038 Holliday junction DNA helicase RuvB (ruvB)
ORF00039 phosphotyrosine protein phosphatase, low molecular weight
ORF00040 MORN motif family protein
ORF00041 membrane protein, putative
ORF00043 alcohol dehydrogenase, propanol-preferring (adhP)
ORF00045 MATE efflux family protein
ORF00046 ribosomal protein S10 (rpsJ)
ORF00047 ribosomal protein L3 (rplC)
ORF00048 ribosomal protein L4 (rplD)
ORF00049-ribosomal protein L23 (rplW)
ORF00050 ribosomal protein L2 (rplB)
ORF00052 ribosomal protein S19 (rpsS)
ORF00054 ribosomal protein L22 (rplV)
ORF00055 ribosomal protein S3 (rpsC)
ORF00056 ribosomal protein L16 (rplP)
ORF00058 ribosomal protein L29 (rpmC)
ORF00059 ribosomal protein S17 (rpsQ)
ORF00060 ribosomal protein L14 (rplN)
ORF00061 ribosomal protein L24 (rplX)
ORF00063 ribosomal protein L5 (rplE)
ORF00065 ribosomal protein S8 (rpsH)
ORF00066 ribosomal protein L6 (rplF)
ORF00068 ribosomal protein L18 (rplR)
ORF00069 ribosomal protein S5 (rpsE)
ORF00070 ribosomal protein L30 (rpmD)
ORF00071 ribosomal protein L15 (rplO)
ORF00072 preprotein translocase, SecY subunit
ORF00073 adenylate kinase (adk)
ORF00074 translation initiation factor IF-1 (infA)
ORF00075 ribosomal protein L36 (rpmJ)
ORF00077 ribosomal protein S13 (rpsM)

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF00078	ribosomal protein S11 (rpsK)
ORF00080	DNA-directed RNA polymerase, alpha subunit (rpoA)
ORF00093	transcriptional regulator ComX1, putative
ORF00094	phosphoglycerate mutase family protein
ORF00097	heat-inducible transcription repressor HrcA (hrcA)
ORF00098	heat shock protein GrpE (grpE)
ORF00099	dnaK protein (dnaK)
ORF00100	dnaJ protein (dnaJ)
ORF00101	transcriptional regulator, GntR family
ORF00102	tRNA pseudouridine synthase A (truA)
ORF00103	phosphomethylpyrimidine kinase, putative
ORF00104	conserved hypothetical protein
ORF00105	conserved hypothetical protein
ORF00106	conserved hypothetical protein
ORF00107	trigger factor (tig)
ORF00108	DNA-directed RNA polymerase, delta subunit, putative
ORF00109	CTP synthase (pyrG)
ORF00111	deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)
ORF00113	carbonic anhydrase-related protein
ORF00115	pyridine nucleotide-disulphide oxidoreductase family protein
ORF00116	glutamyl-tRNA synthetase (gltX)
ORF00119	ribose ABC transporter, ATP-binding protein (rbsA)
ORF00122	ribose operon repressor RbsR (rbsR)
ORF00125	ABC transporter, ATP-binding protein
ORF00126	DNA-binding response regulator
ORF00128	sensor histidine kinase
ORF00131	fructose-bisphosphate aldolase (fba)
ORF00132	L-2-hydroxyisocaproate dehydrogenase
ORF00133	ribosomal protein L28 (rpmB)
ORF00134	conserved hypothetical protein
ORF00135	DAK2 domain protein
ORF00136	expressed SPFH domain/Band 7 family protein
ORF00141	amino acid ABC transporter, ATP-binding protein
ORF00142	amino acid ABC transporter, amino acid-binding protein/permease protein
ORF00143	conserved hypothetical protein
ORF00145	undecaprenol kinase, putative
ORF00146	negative regulator of competence MecA, putative
ORF00149	ABC transporter, ATP-binding protein
ORF00150	conserved hypothetical protein
ORF00151	selenocysteine lyase (csdB)
ORF00152	NifU family protein
ORF00153	conserved hypothetical protein
ORF00155	D-alanyl-D-alanine carboxypeptidase
ORF00158	oligopeptide ABC transporter, permease protein
ORF00160	oligopeptide ABC transporter, ATP-binding protein
ORF00161	oligopeptide ABC transporter, ATP-binding protein
ORF00167	adc operon repressor AdcR (adcR)
ORF00168	zinc ABC transporter, ATP-binding protein
ORF00169	zinc ABC transporter, permease protein
ORF00172	tyrosyl-tRNA synthetase (tyrS)
ORF00173	penicillin-binding protein 1B, putative
ORF00174	DNA-directed RNA polymerase, beta subunit (rpoB)
ORF00176	DNA-directed RNA polymerase beta' subunit (rpoC)
ORF00178	conserved hypothetical protein
ORF00179	competence protein CglA (cglA)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation

ORF00180 competence protein CglB (cglB)
ORF00181 conserved hypothetical protein
ORF00183 conserved hypothetical protein
ORF00184 acetate kinase (ackA)
ORF00190 pyrroline-5-carboxylate reductase (proC)
ORF00191 glutamyl-aminopeptidase (pepA)
ORF00198 single-strand binding protein (ssb)
ORF00211 PTS system, IIBC components
ORF00212 alpha amylase family protein
ORF00214 transcriptional antiterminator, BglG family
ORF00219 PTS system, IIC component, putative
ORF00224 ribosomal protein S15 (rpsO)
ORF00225 polyribonucleotide nucleotidyltransferase (pnp)
ORF00227 serine O-acetyltransferase (cysE)
ORF00229 cysteinyl-tRNA synthetase (cysS)
ORF00230 conserved hypothetical protein
ORF00231 RNA methyltransferase, TrmH family, group 3
ORF00233 DegV family protein
ORF00236 ribosomal protein L13 (rplM)
ORF00237 ribosomal protein S9 (rpsI)
ORF00261 transcriptional regulator MutR family
ORF00262 transporter, putative
ORF00263 amino acid ABC transporter, permease protein
ORF00264 amino acid ABC transporter, amino acid-binding protein
ORF00265 amino acid ABC transporter, permease protein
ORF00266 amino acid ABC transporter, ATP-binding protein
ORF00295 N-acetylglucosamine-6-phosphate deacetylase (nagA)
ORF00296 conserved hypothetical protein
ORF00297 glycyl-tRNA synthetase, alpha subunit (glyQ)
ORF00299 glycyl-tRNA synthetase, beta subunit (glyS)
ORF00300 conserved hypothetical protein
ORF00302 glycerol kinase (glpK)
ORF00303 alpha-glycerophosphate oxidase
ORF00304 glycerol uptake facilitator protein (glpF)
ORF00306 conserved hypothetical protein
ORF00307 transketolase (tkt)
ORF00309 ABC transporter, ATP-binding protein
ORF00310 membrane protein, putative
ORF00313 PTS system, IIBC components
ORF00314 glutamate 5-kinase (proB)
ORF00315 gamma-glutamyl phosphate reductase (proA)
ORF00316 conserved hypothetical protein TIGR00006
ORF00318 penicillin-binding protein 2X (pbpX)
ORF00319 phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY)
ORF00320 ATP-dependent RNA helicase, DEAD/DEAH box family
ORF00321 ABC transporter, substrate-binding protein
ORF00322 amino acid ABC transporter, permease protein
ORF00323 amino acid ABC transporter, ATP-binding protein
ORF00325 thioredoxin reductase (trxB)
ORF00326 conserved hypothetical protein
ORF00327 NAD synthetase (nadE)
ORF00328 aminopeptidase C (pepC)
ORF00329 penicillin-binding protein 1A (pbp1A)
ORF00330 recombination protein U (recU)
ORF00331 conserved hypothetical protein

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF00335 conserved hypothetical protein
ORF00336 conserved hypothetical protein
ORF00337 autoinducer-2 production protein LuxS (luxS)
ORF00338 KH domain protein
ORF00348 guanylate kinase (gmk)
ORF00349 DNA-directed RNA polymerase, omega subunit, putative
ORF00350 primosomal protein N' (priA)
ORF00351 methionyl-tRNA formyltransferase (fmt)
ORF00352 Sun protein (sun)
ORF00353 serine/threonine phosphatase, putative
ORF00354 serine/threonine protein kinase
ORF00355 conserved hypothetical protein
ORF00356 sensor histidine kinase, putative
ORF00358 DNA-binding response regulator
ORF00359 hydrolase, haloacid dehalogenase family/peptidyl-prolyl cis-trans isomerase, cyclophilin type
ORF00360 general stress protein, putative
ORF00361 pyruvate formate-lyase-activating enzyme (pflA)
ORF00362 transcriptional regulator, DeoR family
ORF00363 transcriptional regulator, putative
ORF00364 PTS system, cellobiose-specific IIA component (celC)
ORF00366 PTS system, cellobiose-specific IIB component (celA)
ORF00367 PTS system, cellobiose-specific IIC component (celB)
ORF00368 formate acetyltransferase (pflD)
ORF00369 transaldolase family protein
ORF00371 glycerol dehydrogenase (gldA)
ORF00372 cysteine synthase A (cysK)
ORF00373 conserved hypothetical protein TIGR00257
ORF00374 helicase, putative
ORF00375 competence protein F, putative
ORF00376 ribosomal subunit interface protein (yfiA)
ORF00385 enoyl-CoA hydratase/isomerase family protein
ORF00386 transcriptional regulator, MarR family
ORF00387 3-oxoacyl-(acyl-carrier-protein) synthase III (fabH)
ORF00388 acyl carrier protein (acpP)
ORF00390 enoyl-(acyl-carrier-protein) reductase II (fabK)
ORF00391 malonyl CoA-acyl carrier protein transacylase (fabD)
ORF00392 3-oxoacyl-[acyl-carrier protein] reductase (fabG)
ORF00393 3-oxoacyl-(acyl-carrier-protein) synthase II (fabF)
ORF00394 acetyl-CoA carboxylase, biotin carboxyl carrier protein (accB)
ORF00395 (3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase (fabZ)
ORF00396 acetyl-CoA carboxylase, biotin carboxylase (accC)
ORF00397 acetyl-CoA carboxylase, carboxyl transferase, beta subunit (accD)
ORF00398 acetyl-CoA carboxylase, carboxyl transferase, alpha subunit (accA)
ORF00400 seryl-tRNA synthetase (serS)
ORF00403 conserved hypothetical protein
ORF00404 PTS system, mannose-specific IID component
ORF00405 PTS system, mannose-specific IIC component (manM)
ORF00406 PTS system, mannose-specific IIAB components (manL)
ORF00407 hydrolase, haloacid dehalogenase-like family
ORF00410 xanthine/uracil permease family protein
ORF00411 conserved hypothetical protein TIGR00150, putative
ORF00412 acetyltransferase, GNAT family
ORF00413 expressed protein of unknown function
ORF00415 HIT family protein (hit)
ORF00419 ABC transporter, ATP-binding protein

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF00421	ABC transporter, permease protein
ORF00422	conserved hypothetical protein
ORF00423	conserved hypothetical protein TIGR00091
ORF00424	conserved hypothetical protein, POINT MUTATION
ORF00425	N utilization substance protein A (nusA)
ORF00426	conserved hypothetical protein
ORF00427	ribosomal protein L7A family
ORF00428	translation initiation factor IF-2
ORF00429	ribosome-binding factor A (rbfA)
ORF00432	copper-transporter ATPase CopA
ORF00435	hydrolase, haloacid dehalogenase-like family
ORF00436	DNA polymerase I (polA)
ORF00437	CoA binding domain protein
ORF00440	DNA-binding response regulator
ORF00441	sensor histidine kinase
ORF00443	queuine tRNA-ribosyltransferase (tgt)
ORF00444	conserved hypothetical protein
ORF00449	glucose-6-phosphate isomerase (pgi)
ORF00451	rhomboid family protein
ORF00452	expressed putative lipoprotein
ORF00453	UTP-glucose-1-phosphate uridylyltransferase (galU)
ORF00454	glycerol-3-phosphate dehydrogenase (NAD(P)+) (gpsA)
ORF00455	ribonuclease P protein component (rnpA)
ORF00456	SpolIJ family protein
ORF00458	R3H domain protein
ORF00463	conserved hypothetical protein
ORF00464	RecX protein
ORF00465	RNA methyltransferase, TrmA family
ORF00470	ribonucleoside-diphosphate reductase 2, beta subunit (nrdF)
ORF00472	ribonucleoside-diphosphate reductase 2, alpha subunit (nrdE)
ORF00482	alcohol dehydrogenase, zinc-containing
ORF00483	oxidoreductase, aldo/keto reductase family
ORF00484	cation efflux system protein
ORF00485	transcriptional regulator, TetR family
ORF00496	conserved hypothetical protein
ORF00500	acetyltransferase, GNAT family
ORF00501	conserved hypothetical protein
ORF00502	valyl-tRNA synthetase (valS)
ORF00508	aspartate--ammonia ligase (asnA)
ORF00511	type II DNA modification methyltransferase, putative
ORF00513	phosphopantetheine adenylyltransferase (coaD)
ORF00515	conserved hypothetical protein
ORF00519	conserved hypothetical protein
ORF00520	conserved hypothetical protein TIGR00048
ORF00522	ABC transporter, ATP-binding/permease protein
ORF00523	ABC transporter, ATP-binding/permease protein
ORF00524	anthranilate synthase component II (trpG)
ORF00532	endonuclease III (nth)
ORF00534	conserved hypothetical protein
ORF00535	glucokinase (glk)
ORF00536	expressed protein with rhodanese domain
ORF00537	elongation factor Tu family protein
ORF00540	UDP-N-acetylmuramoylalanine--D-glutamate ligase (murD)
ORF00541	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (murG)

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF00542 cell division protein DivIB, putative
ORF00544 cell division protein FtsA (ftsA)
ORF00545 cell division protein FtsZ (ftsZ)
ORF00546 ylmE protein, putative
ORF00547 ylmF protein (ylmF)
ORF00549 ylmH protein (ylmH)
ORF00550 cell division protein DivIVA, putative
ORF00552 isoleucyl-tRNA synthetase (ileS)
ORF00553 conserved hypothetical protein
ORF00554 MutT/nudix family protein
ORF00555 ATP-dependent Clp protease, ATP-binding subunit
ORF00557 conserved hypothetical protein
ORF00558 amino acid ABC transporter, permease protein
ORF00559 amino acid ABC transporter, ATP-binding protein
ORF00560 phosphoglucomutase/phosphomannomutase family protein
ORF00562 methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase (folD)
ORF00564 exodeoxyribonuclease VII, large subunit (xseA)
ORF00566 geranyltranstransferase, putative
ORF00567 hemolysin A
ORF00570 DNA repair protein RecN (recN)
ORF00571 expressed DegV family protein
ORF00574 DNA-binding protein HU (hup)
ORF00576 dihydroorotate dehydrogenase A (pyrDA)
ORF00577 beta-lactam resistance factor (fibB)
ORF00578 beta-lactam resistance factor (fibA)
ORF00579 murM protein, putative
ORF00580 hydrolase, haloacid dehalogenase-like family
ORF00581 HD domain protein
ORF00582 conserved hypothetical protein
ORF00583 cation-transporting ATPase, E1-E2 family
ORF00588 cell division ABC transporter, ATP-binding protein FtsE (ftsE)
ORF00589 cell division ABC transporter, permease protein FtsX (ftsX)
ORF00591 metallo-beta-lactamase superfamily protein
ORF00593 DNA polymerase III, epsilon subunit/ATP-dependent helicase DinG
ORF00595 aspartate aminotransferase (aspC)
ORF00596 asparaginyl-tRNA synthetase (asnS)
ORF00601 conserved hypothetical protein
ORF00602 conserved hypothetical protein
ORF00603 conserved hypothetical protein
ORF00605 zinc ABC transporter, zinc-binding adhesion lipoprotein
ORF00606 ribosomal protein L31 (rpmE)
ORF00607 DHH family protein
ORF00609 flavodoxin
ORF00614 ribosomal protein L19 (rplS)
ORF00640 prophage LambdaSa1, single-strand binding protein (ssb)
ORF00693 DNA-binding response regulator VncR (vncR)
ORF00694 sensor histidine kinase VncS (vncS)
ORF00699 rod shape-determining protein RodA, putative (rodA)
ORF00700 hydrolase, haloacid dehalogenase-like family
ORF00701 DNA gyrase, B subunit (gyrB)
ORF00702 septation ring formation regulator EzrA, putative
ORF00705 conserved hypothetical protein
ORF00706 enolase (eno)
ORF00708 3-phosphoshikimate 1-carboxyvinyltransferase (aroA)
ORF00709 shikimate kinase (aroK)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation

ORF00710	psr protein
ORF00711	RNA methyltransferase, TrmA family
ORF00729	sortase family protein
ORF00731	sortase family protein
ORF00734	sortase family protein, FRAMESHIFT
ORF00743	ABC transporter, ATP-binding protein
ORF00744	membrane protein
ORF00745	conserved hypothetical protein
ORF00748	cylG protein (cylG)
ORF00776	DNA-entry nuclease, putative
ORF00789	2-keto-3-deoxygluconate kinase
ORF00792	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase (eda)
ORF00798	proline dipeptidase (pepQ)
ORF00799	transcriptional regulator, RegM family
ORF00802	glycosyl transferase, group 1 family protein
ORF00803	threonyl-tRNA synthetase (thrS)
ORF00804	DNA-binding response regulator
ORF00808	amino acid ABC transporter, permease protein
ORF00810	amino acid ABC transporter, ATP-binding protein
ORF00811	DNA-binding response regulator
ORF00812	sensory box histidine kinase
ORF00813	metallo-beta-lactamase family protein
ORF00815	ribonuclease III (rnc)
ORF00816	expressed putative chromosome segregation SMC protein
ORF00817	hydrolase, haloacid dehalogenase-like family
ORF00818	hydrolase, haloacid dehalogenase-like family
ORF00819	signal recognition particle-docking protein FtsY (ftsY)
ORF00820	ABC transporter, substrate-binding protein
ORF00821	ABC transporter, permease protein, putative
ORF00824	transcriptional accessory protein Tex, putative
ORF00825	conserved hypothetical protein
ORF00828	HPr(Ser) kinase/phosphatase (hprK)
ORF00830	prolipoprotein diacylglycerol transferase (lgt)
ORF00832	conserved hypothetical protein
ORF00835	peptidase, U32 family, putative
ORF00836	peptidase, U32 family
ORF00837	conserved hypothetical protein
ORF00844	lysyl-tRNA synthetase (lysS)
ORF00846	phosphoglycerate mutase family protein
ORF00847	ebsC family protein, putative
ORF00850	peptidase, U32 family
ORF00855	oligoendopeptidase F, putative
ORF00856	phosphoenolpyruvate carboxylase (ppc)
ORF00859	cell division protein, FtsW/RodA/SpoVE family (ftsW)
ORF00861	translation elongation factor Tu (tuf)
ORF00863	triosephosphate isomerase (tpiA)
ORF00865	phosphoglycerate mutase (gpmA)
ORF00867	recombination protein RecR (recR)
ORF00868	D-alanine--D-alanine ligase
ORF00869	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase (murF)
ORF00870	oxalate:formate antiporter
ORF00871	membrane protein, putative
ORF00873	peptide chain release factor 3 (prfC)
ORF00876	ABC transporter, ATP-binding protein
ORF00880	ATP-dependent RNA helicase, DEAD/DEAH box family

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF00882 conserved hypothetical protein
ORF00883 conserved hypothetical protein
ORF00884 acyltransferase family protein
ORF00885 competence protein CeiA (ceiA)
ORF00887 DNA internalization-related competence protein ComEC/Rec2
ORF00889 sugar-binding transcriptional regulator, LacI family
ORF00892 DNA polymerase III, delta subunit, putative□
ORF00893 superoxide dismutase, Fe-Mn (sodA)
ORF00894 transcriptional antiterminator LicT
ORF00895 PTS system, beta-glucosides-specific IIABC components
ORF00896 6-phospho-beta-glucosidase (bglA)
ORF00899 glycerate kinase 2 (gark)
ORF00904 S-adenosylmethionine:tRNA ribosyltransferase-isomerase (queA)
ORF00906 glucosamine-6-phosphate isomerase (nagB)
ORF00908 ribosomal small subunit pseudouridine synthase
ORF00911 competence protein CoiA (coiA)
ORF00912 oligoendopeptidase B (pepB)
ORF00914 O-methyltransferase family protein
ORF00916 protease maturation protein, putative
ORF00919 alanyl-tRNA synthetase (alaS)
ORF00925 transcriptional regulator, Cro/Ci family
ORF00928 ribonucleoside-diphosphate reductase 2, beta subunit (nrdF)
ORF00929 ribonucleoside-diphosphate reductase 2, alpha subunit (nrdE)
ORF00930 ribonucleoside-diphosphate reductase 2, NrdH-redoxin (nrdH)
ORF00931 phosphocarrier protein HPr (ptsH)
ORF00932 phosphoenolpyruvate-protein phosphotransferase (ptsI)
ORF00933 glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent (gapN)
ORF00934 polysaccharide deacetylase family protein
ORF00935 ATP-dependent RNA helicase, DEAD/DEAH box family
ORF00936 uridine kinase (udk)
ORF00937 conserved hypothetical protein
ORF00938 DNA polymerase III, gamma and tau subunits (dnaX)
ORF00940 biotin--acetyl-CoA-carboxylase ligase
ORF00941 S-adenosylmethionine synthetase (metK)
ORF00955 UDP-N-acetylglucosamine 1-carboxyvinyltransferase (murA)
ORF00956 acetyltransferase, GNAT family
ORF00957 CBS domain protein
ORF00958 methionine aminopeptidase, type I (map)
ORF00959 ribonuclease BN, putative
ORF00962 conserved hypothetical protein
ORF00963 DNA ligase, NAD-dependent (ligA)
ORF00964 BmrU protein, putative
ORF00966 pullulanase, putative
ORF00973 ATP synthase F0, A subunit (atpB)
ORF00974 ATP synthase F0, B subunit (atpF)
ORF00975 ATP synthase F1, delta subunit (atpH)
ORF00976 ATP synthase F1, alpha subunit (atpA)
ORF00977 ATP synthase F1, gamma subunit (atpG)
ORF00978 ATP synthase F1, beta subunit (atpD)
ORF00979 ATP synthase F1, epsilon subunit (atpC)
ORF00981 UDP-N-acetylglucosamine 1-carboxyvinyltransferase (murA)
ORF00983 DNA-entry nuclease (endA)
ORF00984 phenylalanyl-tRNA synthetase, alpha subunit (pheS)
ORF00986 phenylalanyl-tRNA synthetase, beta subunit (pheT)
ORF00988 exonuclease RexB (rexB)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation

ORF00989	exonuclease RexA (rexA)
ORF00991	tRNA modification GTPase TrmE (trmE)
ORF00992	ABC transporter, ATP-binding protein
ORF00993	acetoin dehydrogenase, thymine PPi dependent, E1 component, alpha subunit
ORF00994	acetoin dehydrogenase, thymine PPi dependent, E1 component, beta subunit
ORF00995	acetoin dehydrogenase, thymine PPi dependent, E2 component, dihydrolipoamide
ORF00996	acetoin dehydrogenase, thymine PPi dependent, E3 component, dihydrolipoamide dehydrogenase
ORF00997	lipoate-protein ligase A (lplA)
ORF00998	cobyrinic acid synthase, putative
ORF00999	mur ligase family protein
ORF01000	conserved hypothetical protein TIGR00159
ORF01001	expressed protein of unknown function
ORF01002	phosphoglucosyltransferase/phosphomannosyltransferase family protein
ORF01005	oxygen-independent coproporphyrinogen III oxidase, putative
ORF01006	conserved hypothetical protein
ORF01007	hydrolase, haloacid dehalogenase-like family
ORF01008	conserved hypothetical protein
ORF01023	GTP-binding protein LepA (lepA)
ORF01027	PilB-related protein
ORF01030	cation-transporting ATPase, E1-E2 family
ORF01033	conserved hypothetical protein
ORF01040	Tn916, tetracycline resistance protein (tetM)
ORF01057	transcriptional regulator, GntR family
ORF01058	DNA polymerase III, alpha subunit (dnaE)
ORF01059	6-phosphofructokinase (pfk)
ORF01060	pyruvate kinase (pyk)
ORF01063	glucosamine-fructose-6-phosphate aminotransferase (isomerizing) (glmS)
ORF01066	phnA protein (phnA)
ORF01068	amino acid ABC transporter, permease protein
ORF01069	amino acid ABC transporter, ATP-binding protein
ORF01070	amino acid ABC transporter, amino acid-binding protein
ORF01072	ribosomal protein S20 (rpsT)
ORF01073	pantothenate kinase (coaA)
ORF01074	conserved hypothetical protein
ORF01075	cytidine deaminase (cdd)
ORF01076	expressed putative lipoprotein
ORF01077	sugar ABC transporter, ATP-binding protein
ORF01078	sugar ABC transporter, permease protein, putative
ORF01079	sugar ABC transporter, permease protein, putative
ORF01080	NADH oxidase (nox-2)
ORF01081	L-lactate dehydrogenase (ldh)
ORF01082	DNA gyrase, A subunit (gyrA)
ORF01083	sortase SrtA (srtA)
ORF01089	GMP synthase (guaA)
ORF01090	transcriptional regulator, GntR family
ORF01091	gid protein (gid)
ORF01093	expressed putative lipoprotein
ORF01097	ABC transporter, ATP-binding protein
ORF01099	DNA-binding response regulator
ORF01101	site-specific recombinase, phage integrase family
ORF01106	signal recognition particle protein Ffh (ffh)
ORF01108	conserved hypothetical protein
ORF01109	sensor histidine kinase CiaH
ORF01110	DNA-binding response regulator CiaR (ciaR)
ORF01111	aminopeptidase N (pepN)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation

ORF01112 phosphate transport system regulatory protein PhoU (phoU)
ORF01113 phosphate ABC transporter, ATP-binding protein PstB, putative
ORF01114 phosphate ABC transporter, ATP-binding protein PstB, putative
ORF01115 phosphate ABC transporter, permease protein PstA, putative
ORF01116 phosphate ABC transporter, permease protein
ORF01117 phosphate ABC transporter, phosphate-binding protein
ORF01118 NOL1/NOP2/sun family protein
ORF01119 inositol monophosphatase family protein
ORF01120 conserved hypothetical protein
ORF01121 conserved hypothetical protein
ORF01122 macrolide-efflux protein mreA/riboflavin biosynthesis protein RibF
ORF01123 tRNA pseudouridine synthase B (truB)
ORF01125 conserved hypothetical protein
ORF01128 permease, putative
ORF01129 ABC transporter, ATP-binding protein
ORF01131 DNA topoisomerase I (topA)
ORF01132 DprA/SMF protein, putative DNA processing factor (dprA)
ORF01134 iron compound ABC transporter, ATP-binding protein
ORF01137 acetyltransferase, CysE/LacA/LpxA/NodL family
ORF01138 ribonuclease HII (rmhB)
ORF01139 GTP-binding protein
ORF01176 carbamoyl-phosphate synthase, large subunit (carB)
ORF01177 carbamoyl-phosphate synthase, small subunit (carA)
ORF01178 aspartate carbamoyltransferase (pyrB)
ORF01179 dihydroorotase, multifunctional complex type (pyrC)
ORF01180 orotate phosphoribosyltransferase (pyrE)
ORF01181 orotidine 5'-phosphate decarboxylase (pyrF)
ORF01183 ABC transporter, ATP-binding protein
ORF01184 ribonucleotide reductase, truncation
ORF01188 cardiolipin synthetase (cls)
ORF01189 formate--tetrahydrofolate ligase (fhs)
ORF01190 lipoate-protein ligase A (lplA)
ORF01198 flavoprotein-related protein
ORF01199 flavoprotein family protein
ORF01200 membrane protein, putative
ORF01201 phosphoglucomutase (pgm)
ORF01203 IS861, transposase OrfB
ORF01205 ABC transporter, ATP-binding/permease protein
ORF01206 ABC transporter, ATP-binding/permease protein
ORF01207 conserved hypothetical protein
ORF01208 conserved hypothetical protein
ORF01209 Serine hydroxymethyltransferase
ORF01210 Sua5/YciO/YrdC/YwlC family protein
ORF01211 modification methylase, HemK family
ORF01212 peptide chain release factor 1 (prfA)
ORF01213 thymidine kinases (tdk)
ORF01214 4-oxalocrotonate tautomerase (xylM)
ORF01216 ApeE family protein
ORF01220 xanthine permease (pbuX)
ORF01221 xanthine phosphoribosyltransferase (xpt)
ORF01222 guanosine monophosphate reductase (guaC)
ORF01227 phosphate acetyltransferase
ORF01228 ribosomal large subunit pseudouridine synthase, RluD subfamily
ORF01229 expressed protein of unknown function
ORF01230 GTP pyrophosphokinase family protein

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF01231 conserved hypothetical protein
ORF01232 ribose-phosphate pyrophosphokinase (prsA)
ORF01233 cysteine desulphurase (iscS)
ORF01234 conserved hypothetical protein
ORF01235 conserved hypothetical protein
ORF01236 DNA repair protein RadC (radC)
ORF01238 6-phospho-beta-glucosidase (ascB)
ORF01239 platelet activating factor, putative
ORF01240 hydrolase, haloacid dehalogenase-like family
ORF01242 voltage-gated chloride channel family protein
ORF01243 spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein (potD)
ORF01244 spermidine/putrescine ABC transporter, permease protein (potC)
ORF01245 spermidine/putrescine ABC transporter, permease protein (potB)
ORF01246 spermidine/putrescine ABC transporter, ATP-binding protein (potA)
ORF01247 UDP-N-acetylenolpyruvoylglucosamine reductase (murB)
ORF01248 2-amino-4-hydroxy-6-hydroxymethylhydropteridine pyrophosphokinase (folK)
ORF01250 dihydropteroate synthase (folP)
ORF01251 GTP cyclohydrolase I (folE)
ORF01252 folypolyglutamate synthase (folC)
ORF01259 aldehyde dehydrogenase family protein
ORF01260 membrane protein
ORF01274 gls24 protein, putative
ORF01276 gls24 protein, putative
ORF01279 conserved hypothetical protein
ORF01282 ATP-dependent DNA helicase PcrA (pcrA)
ORF01283 conserved hypothetical protein, FRAMESHIFT
ORF01284 uracil permease (uraA)
ORF01285 sodium:alanine symporter family protein
ORF01286 cation efflux family protein
ORF01290 ribosomal protein S1 (rpsA)
ORF01292 branched-chain amino acid aminotransferase (ilvE)
ORF01294 DNA topoisomerase IV, A subunit (parC)
ORF01295 DNA topoisomerase IV, B subunit (parE)
ORF01296 membrane protein, putative
ORF01297 uracil-DNA glycosylase (ung)
ORF01317 transcriptional regulator, LysR family, putative
ORF01319 purine nucleoside phosphorylase (deoD)
ORF01321 purine nucleoside phosphorylase (deoD)
ORF01323 phosphopentomutase (deoB)
ORF01324 ribose 5-phosphate isomerase (rpiA)
ORF01327 tributyrin esterase (estA)
ORF01328 metallo-beta-lactamase superfamily protein
ORF01329 ABC transporter, ATP-binding protein
ORF01330 ABC transporter, permease protein
ORF01331 conserved hypothetical protein
ORF01332 adherence and virulence protein A (pavA)
ORF01335 TPR domain protein
ORF01336 membrane protein
ORF01338 mutator MutT protein (mutX)
ORF01339 hyaluronidase
ORF01343 iminodiacetate oxidase, putative
ORF01344 conserved hypothetical protein TIGR00486
ORF01345 conserved hypothetical protein
ORF01346 DNA replication protein Dnad, putative
ORF01347 adenine phosphoribosyltransferase (apt)

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF01350 single-stranded-DNA-specific exonuclease RecJ (recJ)
ORF01351 oxidoreductase, short chain dehydrogenase/reductase family
ORF01352 metallo-beta-lactamase superfamily protein
ORF01353 conserved hypothetical protein
ORF01354 GTP-binding protein HflX (hflX)
ORF01355 tRNA delta(2)-isopentenylpyrophosphate transferase (miaA)
ORF01357 exfoliative toxin A, putative
ORF01358 pullulanase, putative
ORF01362 conserved hypothetical protein
ORF01363 peptidase, M20/M25/M40 family
ORF01364 nitroreductase family protein
ORF01367 excinuclease ABC, C subunit (uvrC)
ORF01380 streptococcal histidine triad family protein
ORF01381 laminin-binding surface protein (lmb)
ORF01397 Tn5252, relaxase
ORF01403 mercuric reductase (merA)
ORF01406 IS861, transposase OrfB, truncation
ORF01407 cation-transporting ATPase, E1-E2 family
ORF01411 conserved hypothetical protein
ORF01412 cation-transporting ATPase, E1-E2 family
ORF01415 transcriptional repressor CopY, putative
ORF01416 cadmium resistance transporter, putative
ORF01451 C-5 cytosine-specific DNA methylase
ORF01453 conserved hypothetical protein
ORF01455 ribosomal protein L7/L12 (rplL)
ORF01456 ribosomal protein L10 (rplJ)
ORF01458 ATP-dependent Clp protease, ATP-binding subunit
ORF01467 GTP-binding protein (cgpA)
ORF01468 ATP-dependent Clp protease, ATP-binding subunit ClpX (clpX)
ORF01470 dihydrofolate reductase (folA)
ORF01471 thymidylate synthase (thyA)
ORF01472 HMG-CoA synthase
ORF01473 3-hydroxy-3-methylglutaryl-CoA reductase
ORF01474 conserved hypothetical protein
ORF01475 hemolysin III, putative
ORF01476 conserved hypothetical protein TIGR00147
ORF01479 isopentenyl-diphosphate delta-isomerase
ORF01480 phosphomevalonate kinase
ORF01481 diphosphomevalonate decarboxylase (mvaD)
ORF01482 mevalonate kinase, putative
ORF01484 DNA-binding response regulator
ORF01491 polypeptide deformylase, putative
ORF01495 ABC transporter, ATP-binding/permease protein
ORF01496 ABC transporter, ATP-binding/permease protein
ORF01498 ABC transporter, ATP-binding protein
ORF01499 polyA polymerase family protein
ORF01500 DegV family protein
ORF01501 expressed protein of unknown function
ORF01504 PTS system, fructose specific IIBC components
ORF01505 1-phosphofructokinase (fruK)
ORF01506 lactose phosphotransferase system repressor (lacR)
ORF01507 beta-lactam resistance factor
ORF01511 pyridine nucleotide-disulphide oxidoreductase family protein
ORF01512 tRNA (guanine-N1)-methyltransferase (trmD)
ORF01513 16S rRNA processing protein RimM (rimM)

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF01515 transcriptional regulator, RofA family
ORF01516 KH domain protein
ORF01517 ribosomal protein S16 (rpsP)
ORF01518 permease, putative
ORF01519 ABC transporter, ATP-binding protein
ORF01520 conserved hypothetical protein
ORF01523 carbamoyl-phosphate synthase, small subunit (carA)
ORF01524 pyrimidine operon regulatory protein (pyrR)
ORF01525 ribosomal large subunit pseudouridine synthase, RluD subfamily
ORF01526 lipoprotein signal peptidase (lspA)
ORF01527 transcriptional regulator, LysR family
ORF01528 ribosomal protein L27 (rpmA)
ORF01529 conserved hypothetical protein
ORF01530 ribosomal protein L21 (rplU)
ORF01531 conserved hypothetical protein, FRAMESHIFT
ORF01532 thiamine biosynthesis protein ThiI (thiI)
ORF01533 cysteine desulphurase (iscS)
ORF01536 glutathione reductase (gor)
ORF01537 conserved hypothetical protein
ORF01538 chorismate synthase (aroC)
ORF01539 3-dehydroquinase synthase (aroB)
ORF01540 3-dehydroquinase dehydratase (aroD)
ORF01541 conserved hypothetical protein
ORF01543 ribosomal protein L20 (rplT)
ORF01544 ribosomal protein L35 (rpmI)
ORF01545 translation initiation factor IF-3 (infC)
ORF01546 cytidylate kinase (cmk)
ORF01548 ferredoxin, 4Fe-4S
ORF01550 peptidase t (pepT)
ORF01551 polysaccharide biosynthesis protein, putative
ORF01552 UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (murE)
ORF01553 iron compound ABC transporter, ATP-binding protein (fepC)
ORF01555 iron compound ABC transporter, permease protein
ORF01556 iron compound ABC transporter, permease protein
ORF01558 inorganic pyrophosphatase, manganese-dependent (ppa)
ORF01559 pyruvate formate-lyase-activating enzyme (pflA)
ORF01560 CBS domain protein
ORF01561 conserved hypothetical protein
ORF01564 PAP2 family protein
ORF01565 membrane protein, putative
ORF01567 expressed sortase family protein
ORF01568 sortase family protein
ORF01571 rogB protein FRAMESHIFT (rogB)
ORF01587 conserved hypothetical protein
ORF01589 RNA polymerase sigma-70 factor (rpoD)
ORF01590 DNA primase (dnaG)
ORF01591 large conductance mechanosensitive channel protein (mscL)
ORF01592 ribosomal protein S21 (rpsU)
ORF01594 amino acid ABC transporter, amino acid-binding protein
ORF01598 rhodanese family protein
ORF01602 glycogen phosphorylase (glgP)
ORF01603 4-alpha-glucanotransferase (malQ)
ORF01604 maltose operon repressor MalR, putative
ORF01605 maltose/maltodextrin ABC transporter, maltose/maltodextrin-binding protein
ORF01606 maltose ABC transporter, permease protein

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF01607	maltose ABC transporter, permease protein
ORF01614	preprotein translocase SecA subunit, putative
ORF01619	preprotein translocase SecY family protein
ORF01634	excinuclease ABC, B subunit (uvrB)
ORF01636	glutamine ABC transporter, glutamine-binding protein/permease protein (glnP)
ORF01637	glutamine ABC transporter, ATP-binding protein, GlnQ putative
ORF01640	GTP-binding protein, GTP1/Obg family (obg)
ORF01646	amidase family protein
ORF01647	ribosomal small subunit pseudouridine synthase A (rsuA)
ORF01648	oxidoreductase, aldo/keto reductase family
ORF01651	lactoylglutathione lyase (gloA)
ORF01652	glycosyl transferase, group 2 family protein
ORF01654	SsrA-binding protein (smpB)
ORF01655	exoribonuclease, VacB/Rnb family (vacB)
ORF01657	preprotein translocase, SecG subunit
ORF01658	multi-drug resistance protein
ORF01662	dephospho-CoA kinase
ORF01663	formamidopyrimidine-DNA glycosylase (mutM)
ORF01677	GTP-binding protein Era (era)
ORF01678	diacylglycerol kinase (dgkA)
ORF01679	conserved hypothetical protein TIGR00043
ORF01685	PhoH family protein
ORF01687	conserved hypothetical protein
ORF01689	conserved hypothetical protein
ORF01690	ribosome recycling factor (frr)
ORF01691	uridylate kinase (pyrH)
ORF01693	peptide ABC transporter, ATP-binding protein FRAMESHIFT
ORF01697	ribosomal protein L1 (rplA)
ORF01698	ribosomal protein L11 (rplK)
ORF01706	IS861, transposase OrfB
ORF01707	chorismate binding enzyme
ORF01708	FtsK/SpoIIIE family protein
ORF01709	peptidyl-prolyl cis-trans isomerase, cyclophilin-type
ORF01710	manganese ABC transporter, permease protein
ORF01711	manganese ABC transporter, ATP-binding protein
ORF01712	manganese ABC transporter, manganese-binding adhesion liprotein
ORF01713	iron-dependent transcriptional regulator
ORF01714	5-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase (pfs)
ORF01716	MutT/nudix family protein
ORF01718	UDP-N-acetylglucosamine pyrophosphorylase (glmU)
ORF01722	oxidoreductase, Gfo/ldh/MocA family
ORF01725	gluconate 5-dehydrogenase, putative
ORF01726	conserved hypothetical protein
ORF01738	branched-chain amino acid transport system II carrier protein (brnQ)
ORF01739	methionyl-tRNA synthetase (metG)
ORF01745	exodeoxyribonuclease (exoA)
ORF01746	conserved hypothetical protein
ORF01752	copper homeostasis protein CutC, putative
ORF01755	tetrapyrrole methylase family protein
ORF01756	conserved hypothetical protein
ORF01758	DNA polymerase III, delta prime subunit, putative
ORF01759	thymidylate kinase (tmk)
ORF01773	ATP-dependent Clp protease, proteolytic subunit ClpP (clpP)
ORF01774	uracil phosphoribosyltransferase (upp)
ORF01777	RNA methyltransferase, TrmH family, group 2

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation

ORF01781 conserved hypothetical protein TIGR00278
ORF01782 ribosomal large subunit pseudouridine synthase B (rluB)
ORF01783 conserved hypothetical protein TIGR00281
ORF01784 conserved hypothetical protein
ORF01785 integrase/recombinase, phage integrase family
ORF01786 CBS domain protein
ORF01787 conserved hypothetical protein
ORF01788 HAM1 protein
ORF01789 glutamate racemase (murl)
ORF01791 membrane protein, putative
ORF01792 transcriptional regulator, biotin repressor family
ORF01793 membrane protein, putative
ORF01795 RNA methyltransferase, TrmH family
ORF01796 acylphosphatase
ORF01797 lipoprotein, putative
ORF01799 amino acid ABC transporter, permease protein
ORF01801 amidase family protein
ORF01802 transcription elongation factor GreA (greA)
ORF01803 conserved hypothetical protein
ORF01804 acetyltransferase, GNAT family
ORF01805 UDP-N-acetylmuramate--alanine ligase (murC)
ORF01806 conserved hypothetical protein
ORF01808 expressed putative helicase
ORF01811 phosphoglycerate dehydrogenase-related protein
ORF01812 primosomal protein Dnal (dnal)
ORF01813 conserved hypothetical protein
ORF01814 conserved hypothetical protein TIGR00244
ORF01815 sensor histidine kinase CsrS (csrS)
ORF01816 DNA-binding response regulator CsrR (csrR)
ORF01817 conserved hypothetical protein
ORF01818 heat shock protein HtpX (htpX)
ORF01820 lemA protein (lemA)
ORF01821 glucose-inhibited division protein B (gidB)
ORF01822 sodium transport family protein
ORF01823 potassium uptake protein, Trk family, putative
ORF01825 ABC transporter, ATP-binding protein
ORF01828 branched-chain amino acid transport system II carrier protein (brnQ)
ORF01829 alcohol dehydrogenase, zinc-containing (adh)
ORF01830 ABC transporter, permease protein
ORF01831 ABC transporter, ATP-binding protein
ORF01833 expressed YaeC family protein
ORF01834 ABC transporter, substrate-binding protein
ORF01835 glutamine amidotransferase, class I
ORF01837 conserved hypothetical protein TIGR01033
ORF01846 glycerol uptake facilitator protein (glpF)
ORF01849 conserved hypothetical protein
ORF01851 conserved hypothetical protein
ORF01852 iojap-related protein
ORF01854 conserved hypothetical protein TIGR00488
ORF01855 conserved hypothetical protein TIGR00482
ORF01856 conserved hypothetical protein TIGR00253
ORF01857 GTP-binding protein
ORF01858 hydrolase, haloacid dehalogenase-like family
ORF01860 glutamyl-tRNA(Gln) amidotransferase, B subunit (gatB)
ORF01861 glutamyl-tRNA(Gln) amidotransferase, A subunit (gatA)

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF01862 glutamyl-tRNA(Gln) amidotransferase, C subunit (gatC)
ORF01867 isochorismatase family protein
ORF01869 transcriptional regulator CodY, putative
ORF01870 aminotransferase, class I
ORF01871 universal stress protein family FRAMESHIFT
ORF01872 hydrolase, haloacid dehalogenase-like family
ORF01873 asparaginase family protein
ORF01874 shikimate 5-dehydrogenase (aroE)
ORF01876 ATP-dependent DNA helicase RecG (recG)
ORF01878 alanine racemase (alr)
ORF01879 holo-(acyl-carrier-protein) synthase (acpS)
ORF01881 preprotein translocase, SecA subunit (secA)
ORF01882 mannose-6-phosphate isomerase, class I (manA)
ORF01883 fructokinase (scrK)
ORF01885 PTS system IIBC components
ORF01886 sucrose-6-phosphate hydrolase (scrB)
ORF01887 sucrose operon repressor ScrR (scrR)
ORF01888 N utilization substance protein B (nusB)
ORF01889 conserved hypothetical protein
ORF01890 translation elongation factor P (efp)
ORF01900 cytidine/deoxycytidylate deaminase family protein
ORF01906 excinuclease ABC, A subunit (uvrA)
ORF01907 conserved hypothetical protein
ORF01908 magnesium transporter, CorA family (corA)
ORF01909 ribosomal protein S18 (rpsR)
ORF01910 single-strand binding protein (ssb)
ORF01911 ribosomal protein S6 (rpsF)
ORF01912 A/G-specific adenine glycosylase (mutY)
ORF01914 thioredoxin (trx)
ORF01915 PAP2 family protein
ORF01916 MutS2 family protein
ORF01917 conserved hypothetical protein
ORF01918 conserved hypothetical protein
ORF01919 ribonuclease HIII (rnhC)
ORF01920 signal peptidase I
ORF01921 helicase, putative
ORF01923 DNA-damage inducible protein P (dinP)
ORF01924 formate acetyltransferase (pfID)
ORF01926 conserved hypothetical protein
ORF01927 proteinase, putative, degenerate, FRAMESHIFT
ORF01929 glycerol uptake facilitator protein, putative
ORF01930 universal stress protein family
ORF01933 X-pro dipeptidyl-peptidase (pepX)
ORF01937 ABC transporter, ATP-binding protein CydC (cydC)
ORF01938 ABC transporter, ATP-binding protein CydD
ORF01945 conserved hypothetical protein TIGR00103
ORF01948 exonuclease
ORF01949 conserved hypothetical protein
ORF01950 conserved hypothetical protein TIGR00275
ORF01952 ribosomal protein S14 (rpsN)
ORF01957 O-sialoglycoprotein endopeptidase family protein
ORF01958 ribosomal-protein-alanine acetyltransferase, putative
ORF01960 expressed protein of unknown function
ORF01961 conserved hypothetical protein
ORF01962 metallo-beta-lactamase superfamily protein

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation

ORF01963 conserved hypothetical protein
ORF01964 glutamine synthetase, type I (glnA)
ORF01965 transcriptional regulator GlnR (glnR)
ORF01967 conserved hypothetical protein
ORF01969 phosphoglycerate kinase (pgk)
ORF01971 glyceraldehyde 3-phosphate dehydrogenase (gap)
ORF01972 translation elongation factor G (fusA)
ORF01973 ribosomal protein S7 (rpsG)
ORF01974 ribosomal protein S12 (rpsL)
ORF01975 pur operon repressor (purR)
ORF01976 HD domain protein
ORF01977 conserved hypothetical protein
ORF01978 conserved hypothetical protein
ORF01979 ribulose-phosphate 3-epimerase (rpe)
ORF01980 conserved hypothetical protein TIGR00157
ORF01983 dimethyladenosine transferase (ksgA)
ORF01985 primase-related protein
ORF01987 deoxyribonuclease, TatD family
ORF01992 dltD protein (dltD)
ORF01993 D-alanyl carrier protein (dltC)
ORF01994 dltB protein (dltB)
ORF01996 D-alanine-activating enzyme (dltA)
ORF01997 sensor histidine kinase
ORF01998 DNA-binding response regulator
ORF01999 ribosomal protein L34 (rpmH)
ORF02004 amino acid ABC transporter, ATP-binding protein
ORF02007 conserved hypothetical protein
ORF02008 transcriptional antiterminator, BglG family
ORF02017 sugar binding transcriptional regulator, LacI family
ORF02018 transaldolase family protein
ORF02019 carbohydrate isomerase, AraD/FucA family
ORF02020 hexulose-6-phosphate isomerase, putative
ORF02021 hexulose-6-phosphate synthase, putative
ORF02022 PTS system, IIA component
ORF02023 PTS system, IIB component
ORF02024 transport protein SgaT, putative
ORF02027 adenylosuccinate synthetase (purA)
ORF02033 chaperonin, 33 kDa (hslO)
ORF02034 NifR3/Smm1 family protein
ORF02037 ATP-dependent Clp protease, ATP-binding subunit
ORF02038 transcriptional regulator CtsR (ctsR)
ORF02040 translation elongation factor Ts (tsf)
ORF02041 ribosomal protein S2 (rpsB)
ORF02043 alkyl hydroperoxide reductase, subunit F (ahpF)
ORF02076 prophage LambdaSa2, single-strand binding protein (ssb)
ORF02082 prophage LambdaSa2, type II DNA modification methyltransferase, putative
ORF02086 prophage LambdaSa2, replicative DNA helicase (dnaC)
ORF02104 endopeptidase O (pepO)
ORF02110 polypeptide deformylase (def)
ORF02111 sugar binding transcriptional regulator RegR (regR)
ORF02112 conserved hypothetical protein
ORF02113 PTS system, IID component
ORF02114 PTS system, IIC component
ORF02115 PTS system, IIB component
ORF02116 glucuronidase

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation

ORF02118	PTS system, IIA component
ORF02120	oxidoreductase, short-chain dehydrogenase/reductase family
ORF02121	conserved hypothetical protein
ORF02122	carbohydrate kinase, PfkB family
ORF02123	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase (eda)
ORF02127	DNA polymerase III, alpha subunit, Gram-positive type
ORF02129	prolyl-tRNA synthetase (proS)
ORF02130	membrane-associated zinc metalloprotease, putative
ORF02131	phosphatidate cytidyltransferase (cdsA)
ORF02132	undecaprenyl diphosphate synthase (uppS)
ORF02133	preprotein translocase, YajC subunit (yajC)
ORF02140	glucan 1,6-alpha-glucosidase (dexB)
ORF02141	sugar ABC transporter, ATP-binding protein (msmK)
ORF02142	helix-turn-helix domain protein, fis-type
ORF02144	tagatose 1,6-diphosphate aldolase (lacD)
ORF02145	tagatose-6-phosphate kinase (lacC)
ORF02146	galactose-6-phosphate isomerase, LacB subunit (lacB)
ORF02147	galactose-6-phosphate isomerase, LacA subunit (lacA)
ORF02149	PTS system, IIC component, putative
ORF02150	PTS system, IIB component, putative
ORF02152	PTS system, IIA component, putative
ORF02153	lactose phosphotransferase system repressor (lacR)
ORF02157	adhesion lipoprotein
ORF02158	expressed protein of unknown function TIGR00256
ORF02159	GTP pyrophosphokinase (relA)
ORF02161	nrpI protein (nrpI)
ORF02164	iron ABC transporter, iron-binding protein
ORF02165	DNA-binding response regulator
ORF02167	PTS system, IID component
ORF02168	PTS system, IIC component
ORF02174	ABC transporter, ATP-binding protein
ORF02176	response regulator
ORF02177	conserved hypothetical protein
ORF02178	PTS system, IIABC components
ORF02179	sensor histidine kinase
ORF02180	phosphate regulon response regulator PhoB (phoB)
ORF02182	phosphate ABC transporter, ATP-binding protein (pstB)
ORF02183	phosphate ABC transporter, permease protein
ORF02184	phosphate ABC transporter, permease protein
ORF02188	conserved hypothetical protein TIGR00046
ORF02189	ribosomal protein L11 methyltransferase (prmA)
ORF02197	conserved hypothetical protein
ORF02199	ATPase, AAA family
ORF02249	mercuric reductase (merA)
ORF02272	DNA topology modulation protein FlaR, putative
ORF02273	glycerol dehydrogenase, putative
ORF02281	DNA-binding response regulator
ORF02285	leucyl-tRNA synthetase (leuS)
ORF02290	transcription antitermination protein NusG (nusG)
ORF02293	penicillin-binding protein 2A (pbp2A)
ORF02294	ribosomal large subunit pseudouridine synthase, RluD subfamily
ORF02296	phosphopentomutase (deoB)
ORF02297	deoxyribose-phosphate aldolase (deoC)
ORF02300	uridine phosphorylase (udp)
ORF02302	60 kda chaperonin (groEL)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation

ORF02303 chaperonin, 10 kDa (groES)
ORF02305 ABC transporter, ATP-binding protein
ORF02306 ABC transporter, permease protein
ORF02307 expressed putative lipoprotein
ORF02309 glyoxalase family protein
ORF02310 conserved hypothetical protein
ORF02311 anaerobic ribonucleoside-triphosphate reductase activating protein (nrdG)
ORF02312 acetyltransferase, GNAT family
ORF02315 anaerobic ribonucleoside-triphosphate reductase (nrdD)
ORF02318 conserved hypothetical protein
ORF02320 conserved hypothetical protein
ORF02321 conserved hypothetical protein
ORF02322 recA protein (recA)
ORF02325 DNA-3-methyladenine glycosylase I (tag)
ORF02327 Holliday junction DNA helicase RuvA (ruvA)
ORF02329 DNA mismatch repair protein HexB (hexB)
ORF02333 arginine repressor ArgR, putative
ORF02334 arginyl-tRNA synthetase (argS)
ORF02337 conserved hypothetical protein
ORF02338 conserved hypothetical protein
ORF02339 aspartyl-tRNA synthetase (aspS)
ORF02340 histidyl-tRNA synthetase (hisS)
ORF02342 ribosomal protein L33 (rpmG)
ORF02357 DNA-binding response regulator
ORF02359 membrane protein, putative
ORF02360 carbamate kinase (arcC)
ORF02361 ornithine carbamoyltransferase (argF)
ORF02364 amino acid ABC transporter, ATP-binding protein
ORF02365 amino acid ABC transporter, permease and amino acid-binding protein
ORF02370 membrane protein, putative
ORF02371 transcriptional regulator, TetR family, putative
ORF02373 ribosomal protein S4 (rpsD)
ORF02374 conserved hypothetical protein
ORF02375 replicative DNA helicase (dnaC)
ORF02376 ribosomal protein L9 (rplI)
ORF02377 DHH family protein
ORF02378 glucose inhibited division protein A (gidA)
ORF02380 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (trmU)
ORF02381 L-serine dehydratase, iron-sulfur-dependent, beta subunit (sdhB)
ORF02382 L-serine dehydratase, iron-sulfur-dependent, alpha subunit (sdhA)
ORF02385 cobalt transport family protein
ORF02386 ABC transporter, ATP-binding protein
ORF02387 ABC transporter, ATP-binding protein, FRAMESHIFT
ORF02388 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (pgsA)
ORF02389 peptidase, M16 family
ORF02390 conserved hypothetical protein
ORF02391 conserved hypothetical protein
ORF02392 recF protein (recF)
ORF02396 inosine-5'-monophosphate dehydrogenase (guaB)
ORF02397 transcriptional regulator, ArgR family
ORF02400 arginine deiminase (arcA)
ORF02402 ornithine carbamoyltransferase (argF)
ORF02404 carbamate kinase (arcC)
ORF02405 tryptophanyl-tRNA synthetase (trpS)
ORF02407 conserved hypothetical protein

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF02408 ABC transporter, ATP-binding protein
ORF02409 ABC transporter, permease protein, putative
ORF02410 conserved hypothetical protein TIGR00246
ORF02411 serine protease
ORF02412 partitioning protein, ParB family
ORF02413 chromosomal replication initiator protein DnaA (dnaA)
ORF02415 DNA polymerase III, beta subunit (dnaN)
ORF02417 conserved hypothetical protein
ORF02419 conserved hypothetical GTP-binding protein
ORF02420 peptidyl-tRNA hydrolase (pth)
ORF02421 transcription-repair coupling factor (mfd)
ORF02423 S4 domain protein
ORF02424 cell division protein DivIC, putative
ORF02426 expressed protein of unknown function
ORF02427 MesJ/Ycf62 family protein
ORF02429 cell division protein FtsH (ftsH)

Table 9: GBS genes shared with pneumococcus

ORFxxxxx Annotation

ORF00017	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase (purH)
ORF00025	conserved hypothetical protein
ORF00029	acetyl xylan esterase, putative
ORF00042	aldehyde-alcohol dehydrogenase (adhE)
ORF00044	threonine synthase (thrC)
ORF00081	ribosomal protein L17 (rplQ)
ORF00090	conserved hypothetical protein
ORF00129	argininosuccinate synthase (argG)
ORF00156	oligopeptide ABC transporter, substrate-binding protein, putative
ORF00189	protease, putative
ORF00194	thioredoxin family protein
ORF00195	tRNA binding domain protein
ORF00217	conserved domain protein
ORF00218	PTS system, IIB component, putative
ORF00220	transketolase, N-terminal subunit
ORF00221	transketolase, C-terminal subunit
ORF00223	oxidoreductase, putative
ORF00282	acetyltransferase, GNAT family
ORF00290	IS1381, transposase OrfB
ORF00291	IS1381, transposase OrfA
ORF00293	conserved hypothetical protein
ORF00301	membrane protein, putative
ORF00343	ABC transporter, permease protein, putative
ORF00344	conserved hypothetical protein
ORF00382	aspartate kinase family protein
ORF00399	conserved hypothetical protein
ORF00439	cell wall surface anchor family protein
ORF00447	cytidine/deoxycytidylate deaminase family protein
ORF00450	5-formyltetrahydrofolate cyclo-ligase family protein
ORF00480	transcriptional regulator, MerR family
ORF00499	acetyltransferase, GNAT family
ORF00504	magnesium transporter, CorA family
ORF00521	VanZF domain protein
ORF00612	IS1381, transposase OrfA
ORF00613	IS1381, transposase OrfB
ORF00690	transmembrane protein Vexp1 (vex1)
ORF00691	ABC transporter, ATP-binding protein Vexp2 (vex2)
ORF00692	transmembrane protein Vexp3 (vex3)
ORF00714	conserved hypothetical protein
ORF00732	expressed cell wall surface anchor family protein, putative
ORF00774	ABC transporter, ATP-binding protein
ORF00778	ABC transporter, ATP-binding protein
ORF00780	conserved hypothetical protein
ORF00790	beta-glucuronidase
ORF00800	alpha amylase family protein
ORF00807	amino acid ABC transporter, permease protein
ORF00809	amino acid ABC transporter, amino acid-binding protein
ORF00814	conserved hypothetical protein
ORF00823	bacterial luciferase family protein
ORF00840	riboflavin biosynthesis protein RibD (ribD)
ORF00841	riboflavin synthase, alpha subunit (ribE)
ORF00842	riboflavin biosynthesis protein RibA (ribA)
ORF00843	riboflavin synthase, beta subunit (ribH)
ORF00866	penicillin-binding protein 2b
ORF00905	membrane protein, putative

Table 9: GBS genes shared with pneumococcus**ORFxxxxx Annotation**

ORF00910 major facilitator family protein
ORF00913 hydrolase, haloacid dehalogenase-like family
ORF00918 conserved hypothetical protein
ORF00945 conserved hypothetical protein
ORF00948 ABC transporter, ATP-binding protein
ORF00952 phosphomethylpyrimidine kinase (thiD)
ORF00953 hydroxyethylthiazole kinase (thiM)
ORF00954 thiamine-phosphate pyrophosphorylase (thiE)
ORF00961 GtrA family protein
ORF00967 1,4-alpha-glucan branching enzyme (glgB)
ORF00968 glucose-1-phosphate adenylyltransferase (glgC)
ORF00971 glycogen synthase (glgA)
ORF00985 acetyltransferase, GNAT family
ORF00990 magnesium transporter, CorA family, putative
ORF01022 nucleoside diphosphate kinase (ndk)
ORF01031 nucleoside diphosphate kinase domain protein
ORF01085 conserved hypothetical protein
ORF01087 IS1381, transposase OrfA
ORF01088 IS1381, transposase OrfB
ORF01098 ABC transporter, permease protein, putative
ORF01100 sensor histidine kinase
ORF01102 ABC transporter, substrate-binding protein
ORF01127 protease, putative
ORF01135 iron compound ABC transporter, permease protein
ORF01136 iron compound ABC transporter, permease protein
ORF01185 aspartate-semialdehyde dehydrogenase (asd)
ORF01217 conserved hypothetical protein
ORF01218 conserved hypothetical protein
ORF01219 formate/nitrite transporter family protein
ORF01226 oxidoreductase, short chain dehydrogenase/reductase family, FRAMESHIFT
ORF01254 homoserine kinase (thrB)
ORF01255 homoserine dehydrogenase (hom)
ORF01264 transcriptional regulator, Cro/CI family
ORF01268 thiol peroxidase (psaD)
ORF01305 glycosyltransferase CpsJ(V) (cpsJ)
ORF01306 glycosyltransferase CpsO(V) (cpsO)
ORF01313 CpsD protein (cpsD)
ORF01314 cpsC protein (cpsC)
ORF01315 capsular polysaccharide biosynthesis protein CpsB (cpsB)
ORF01316 capsular polysaccharide biosynthesis protein CpsA (cpsA)
ORF01326 conserved hypothetical protein
ORF01333 alpha-acetolactate decarboxylase (budA)
ORF01334 acetolactate synthase, catabolic (ilvK)
ORF01337 MutT/nudix family protein
ORF01369 MATE efflux family protein
ORF01398 Tn5252, Orf 9 protein
ORF01399 Tn5252, Orf 10 protein
ORF01446 protease, putative
ORF01447 conserved hypothetical protein
ORF01449 conserved hypothetical protein
ORF01492 NADP-specific glutamate dehydrogenase (gdhA)
ORF01569 expressed cell wall surface anchor family protein
ORF01570 cell wall surface anchor family protein
ORF01574 polysaccharide biosynthesis protein
ORF01579 nucleotidyl transferase, putative